

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
1 April 2004 (01.04.2004)

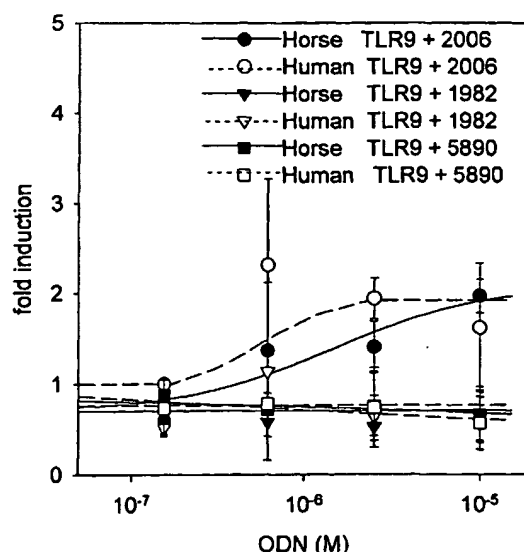
PCT

(10) International Publication Number  
**WO 2004/026888 A2**

- (51) International Patent Classification<sup>7</sup>: **C07H**
- (21) International Application Number:  
PCT/US2003/029577
- (22) International Filing Date:  
19 September 2003 (19.09.2003)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:  
60/412,479 19 September 2002 (19.09.2002) US
- (71) Applicants (for all designated States except US): **COLEY PHARMACEUTICAL GMBH** [DE/DE]; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). **UNIVERSITY OF SASKATCHEWAN** [CA/CA]; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). **QIAGEN GMBH** [DE/DE]; Max-Volmer-Strasse 4, 40724 Hilden (DE).
- (72) Inventors; and  
(75) Inventors/Applicants (for US only): **LIPFORD, Grayson, B.** [US/US]; 38 Bates Road, Watertown, MA 02472 (US). **MOOKHERJEE, Neeloffer** [IN/CA]; Apt 408, 2233 Allison Road., Vancouver, BC V6T 1T7 (CA). **BABIUK, Lorne** [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). **BROWNIE, Robert** [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). **GRIEBEL, Philip** [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). **MUTWIRI, George** [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). **HECKER, Rolf** [DE/DE]; Benrodestr. 60, 40597 Düsseldorf (DE).
- (74) Agent: **STEELE, Alan, W.**; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).
- (81) Designated States (national): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.

WO 2004/026888 A2



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— *without international search report and to be republished upon receipt of that report*

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

### Background of the Invention

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory  
5 CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune  
system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001)  
*Vaccine* 19:618-22. A wide variety of CpG-containing sequences have been screened for  
biological activity and it is reported that optimal CpG DNA sequences can vary among  
species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.

10 Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN.  
Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9  
recognizes CpG DNA is not understood.

### Summary of the Invention

15 Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal  
in response to CpG DNA. To date, the amino acid sequences only of human and murine  
TLR9 have been reported, and, interestingly, these two species are known to prefer different  
CpG motifs. The structural basis for this species-specific CpG motif preference has not yet  
been fully elucidated. The instant invention provides, in part, novel amino acid and  
20 nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are  
useful for elucidating certain key structural features of TLR9. Specifically, comparison of  
sequences of murine, human, and these novel TLR9 sequences permits identification of areas  
of highly conserved sequence, areas of group conservation, and areas of hypervariability. In  
addition, such comparisons permit an assessment of evolutionary relatedness among TLR9  
25 molecules of the various species, as well as an assessment of inter-species homologies.  
Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9  
that may be involved in the CpG binding site, as well as amino acids involved in conferring  
species specificity for particular CpG motifs. Such information may be used to design and  
construct novel TLR9 molecules which incorporate specific point or regional mutations and  
30 which possess desired ligand binding characteristics. Such information may also be useful in  
designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an  
5 extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

10 In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand,  
15 such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID  
20 NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid  
25 molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the  
30 invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a

- 3 -

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided  
5 by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to  
10 one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments  
15 the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the  
20 first species. The method involves aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the  
25 first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b)  
30 differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

- 4 -

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

- 5 -

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment  
10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide  
15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in  
20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
25	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
30	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
35	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTTGATGTT (SEQ ID NO:55),  
 TCCATGACGTATTTGATGTT (SEQ ID NO:56), and  
 TCCATGACGTGTTTGATGTT (SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes  
 5 expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one  
 embodiment the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B. In one  
 embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or  
 CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test  
 10 compounds. In one embodiment the response mediated by the TLR9 signal transduction  
 pathway is measured quantitatively and the response mediated by the TLR9 signal  
 transduction pathway associated with each of the plurality of test compounds is compared  
 with a response arising as a result of an interaction between the functional TLR9 and a  
 reference immunostimulatory compound.

15

### Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid  
 sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig  
 (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid  
 20 sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9  
 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and  
 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six  
 sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and  
 human TLR9 sequences alone.

25 Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine,  
 porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected  
 oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

30

### Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9  
 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key  
 features of the primary sequences of these and related TLR molecules, including previously



- 7 -

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands. Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

- 8 -

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

- 9 -

## SEQ ID NO:1 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI  
HHLHNLDFVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL  
5 SHTNIIIVLDASSLAGLHSLRVLFMDGNCYYNPCNGAVNVTPDAFLGLSNLTHLSLKYNLNLTEVPRQLPPSLEYL  
LLSYNLIIVKGAEDLANLTSIRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSLSLSLN  
SKWFQGLANLSVLDLSENFLYESINKTSFAQNLTRLRKLDLSFNCKKVSFARLHLASSFKSLVSLQELNMNGIF  
FRLNKNLTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVPW  
PASLTPALPSTPVSKNFMVRCKNLRFMTDLNRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
10 VLDLSYNKLDLYHKSFSFELPQLQALDLSYNSQPFMSQIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
VEYLDGSGNGVGRMWDEEDLYLYFFQDLRLSLIHLDSLQNKHLILRPQNLNYLPKSLTKLSFRDNHLSFFNWSSLA  
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
MNLTVLDVSSNPLHCACGAPFVDLLELVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGSL  
AVAVGTVLPLQLHLCGWDVWYCFHLCLAWPLLTRGRSAQALPYDAFVFDKAQSAVADWVYNELRVRLERRG  
15 RRALRLCLEDRDWLPQTLFENLWASIYGRKTLFVLAHTDKVSGLLRSTFLLAQQRLLLEDKDVVVLVILRPDA  
HRSRYVRLRQLCRQSVLFWPHQPNQGQSFWAQLSTALTRDNHNFYNNRNFRCGPAT

## SEQ ID NO:2 (Rat TLR9)

MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI  
HHLHNLDFVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL  
20 SHTNIIIVLDASSLAGLHSLRVLFMDGNCYYNPCNGAVNVTPDAFLGLSNLTHLSLKYNLNLTEVPRQLPPSLEYL  
LLSYNLIIVKGAEDLANLTSIRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSLSLSLN  
SKWFQGLANLSVLDLSENFLYESINKTSFAQNLTRLRKLDLSFNCKKVSFARLHLASSFKSLVSLQELNMNGIF  
FRLNKNLTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVPW  
25 PASLTPALPSTPVSKNFMVRCKNLRFMTDLNRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK  
VLDLSYNKLDLYHKSFSFELPQLQALDLSYNSQPFMSQIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS  
VEYLDGSGNGVGRMWDEEDLYLYFFQDLRLSLIHLDSLQNKHLILRPQNLNYLPKSLTKLSFRDNHLSFFNWSSLA  
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV  
MNLTVLDVSSNPLHCACGAPFVDLLELVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG  
30

## SEQ ID NO:3 (Rat TLR9)

atggttctctgtcgcaggaccctgcaccccttgctctctcctggtacaggccgcagtgctggctgaggctctggcc  
ctgggtaccctgcctgccttctaccctgtgaactgaagcctcatggcctggttagactgcaactggctcttctg  
aagtctgtgcctcacttctctgcccgcagaaccccggtccaacatcaccagccttctcttgatcgccaaccgcac  
35 caccactgcacaacctgcacttctgctccactgcccacgtgcgacagctgaacctcaagtggaaactgtccgccc  
cctggcctcagccctgtcacttctcctgcccgcagacttagaccattgagcccaaaccttctggtctatgcgcatgctg  
gaagagctgaacctgagctataaacggtatcaccactgtgccccgcctgcccagctcctctgacgaatctgagccta  
agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac  
40 gggaaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgagcgccttctggtgcttagcaac  
ctcaccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccagcctggagtagctc  
ctgctgtcctataacctcatcgtaagctgggggcccgaagacctagccaacctgacctcccttcgaatgcttgat  
gtgggtgggaattgcccgtcgctgtgatcacgccccgacctctgtacagaatgcccggcagaagtcccttgatctg  
caccctcagactttccatcacctgagccaccttgaggcctggtgctgaaggacagttctctccactcgctgaac  
45 tccaagtgggtccagggtctggcgaacctctcggtgctggacctgaagcgagaacttctctacgagagcatcaac  
aaaaccagcgcccttcagaacctgacctgtctgcgcaagctcgacctgtccttcaattactgcaagaaggtatcg  
ttcgcccgctccacctggcaagttccttcaagagcctggtgctcgctgcaggagctgaacatgaacggcatcttc  
ttccgcttactcaacaagaacagctcaggtggctggctggtctgcccagctccacacgctgcaccttcaaatg  
aatttcatcaaccaggcgcagctcagcgtctttagtaccttccgagcccttcgcttctgtggacctgtccaataat  
50 cgcacacagcggcctccaacgctgtccagagtcgccccgaaaaggcagacgaggcgaggagggttccatgg  
cctgcaagtctcaccctcagctctcccagcactcccgctctcaagaacttcatggtcaggtgtaagaacctcaga  
ttcaccatggacctgtctcggaacaacaggtgacttcaagccagagatgttcgctcaaccttccatctccag  
tgtctgagcctgagccacaactgcacgcagctgtcgaatggctctcagttcctgcccgtgaccaacctgaag  
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgcttcagtgagctccacaggtgcaggcc

- 10 -

ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg  
tccagggttacagaaccttagcctggcacacaatgacattcacagccgcgtgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtggccgcgtgtgggacgaggaggacctttacctctattttcttc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac  
5 tactctcccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagctctggcc  
ttcctgccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcacccctgccta  
ggcacgctcctccagaaactggatgtcagtagcaacagtatcgtctttgtggtccagccttctttgctctggcg  
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggttgggcccattgtg  
10 atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcacctttgtagacttactg  
ctggaagtgcagaccaaggtgcctggcctgacgggtggaagtgtggcagtcctcccgccagctgcaggggccgc  
agcatctttgcgcaagacctgcggtgtgacctggatgacgtcctttctcgggactgctttggcctttcactcctg  
gctgtggccgtgggcacgggtgtgaccttactgcagcatctctgcggctgggacgtctggtactgtttccatctg  
tgctggcatggctacctttgctgacctggcggcgccagcgcgaagctctccttatgatgccttcgtggtg  
15 ttcgataaggcgagagcggtgtgctgactgggtgtataacagacttcgagtgccggttagaggagcgggcggt  
cgccgagccctacgcttctgtctgaggagccgagattggctgcctggccagacactcttcgagaacctctgggccc  
tccatctatggcagccgcaagactctgtttgtgctggccacacggacaaggtcagtgccctcctgcgaccagc  
ttcctgctggctcagcagcgctgtgaggagccgcaaggtcagtgccctcctgcgaccagc  
caccgctcccgctacgtgcgactgcgccagcctctgcgccagagtggtgctctctggccccatcagcccaac  
20 gggcagggcagcttctgggcccagctgagtacagccctgactagggacaaccaccacttctataaccggaacttc  
tgccggggacctacagcagaatag

## SEQ ID NO:4 (Rat TLR9)

atggttctctgtgcaggacctgcacccttgtctctcctggtagcggccgagtgctggctgaggtcttggcc  
ctgggtacctgcctgccttccctacctgtgaactgaagcctcatggcctggtagactgcaactggctcttctctg  
25 aagtctgtgcctcacttctctgcccgcagaaccccggttccaacatcaccagcctttccttgatcgccaaccgcac  
caccacctgcacaacctcgactttgtccacctgcccacgtgcgacagctgaacctcaagtggaaactgtccgcc  
cctggcctcagccccttgacttctcctgcgcgcatgaccattgagcccaaaaccttctggctatgcgcatgctg  
gaagagctgaacctgagctataacgggtatcaccactgtgccccgcctgccagctccttgacgaatctgagccta  
30 agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac  
gggaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgagccttctcctgggcttgagcaac  
ctcaccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtacctc  
ctgctgtcctataacctcatcgtaagctggggggcgaagacctagccaacctgacctcccttcgaatgcttgat  
gtgggtgggaattgcccgtcgctgtgatcacgccccgacctctgtacagaatgccggcagaagtccttgatctg  
35 caccctcagactttccatcacctgagccaccttgaaggcctgggtgctgaaggacagttctctccactcgctgaac  
tccaagtgggtccagggtctggcgaacctctcggtgctggacctaaagcgagaactttctctacgagagcatcaac  
aaaaccagcgctttcagaacctgacctgtgcgcaagctcgacctgtccttcaattactgcaagaaggtatcg  
ttcgccgcctccacctggcaagttccttcaagagcctgggtgcgctgcaggagctgaacatgaacggcatcttc  
ttccgcttactcaacaagaacacgctcaggtggctggctggtctgcccaagctccacacgctgcaccttcaaatg  
aatttcatcaaccaggcgagctcagcgtctttagtacctccgagcccttcgctttgtggacctgtccaataat  
40 cgcacagcgggctccaacgctgtccagagtcgccccgaaaaggcagacgagcgaggaaggggtccatgg  
cctgcaagctcacccagctctcccgagcactcccgctcacaagaacttcaggtcaggtgtaagaacctcaga  
ttcaccatggacctgtctcggaacaaccagggtgactatcaagccagagatgttcgtcaacctctcccatctccag  
tgtctgagcctgagccacaactgcatcgcgaggtgtcaatggctctcagttcctgcccgtgaccaacctggaag  
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgttcagtgagctcccacagttgcaggcc  
45 ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg  
tccagggttacagaaccttagcctggcacacaatgacattcacagccgcgtgtcctcacgcctctacagcacctca  
gtggagtatctggacttcagcggcaacgggtgtggccgcgtgtgggacgaggaggacctttacctctattttcttc  
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac  
50 tactcccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagctctggcc  
ttcctgccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcacccctgccta  
ggcacgctcctccagaaactggatgtcagtagcaacagtatcgtctttgtggtccagccttctttgctctggcg  
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggttgggcccattgtg  
atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcacctttgtagacttactg  
ctggaagtgcagaccaaggtgcctggcctggctaacgggtgtgaagtgtggcagtcctcccgagctgcagggccgc  
55 agcatctttgcgcaagacctgcggtgtgcctggatgacgtcctttctcgggactgctttggc

- 11 -

## SEQ ID NO:5 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRLPAPFLPCELOPHGLVNCNWFLKSVPHFSAAAPRANVTSLSLLSNRIH  
 HLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS  
 RTNIVLVDPTHTLGLHALRYLYMDGNCYKNPCQGALEVVPGALLGLGNLTHLSLKYNLLEVPRLPPSLETLL  
 5 LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGLVLKDSLYNLDT  
 RWFRGLDRLQVLDLSENFLYDCITKTTFQGLARLRLSNLSFNHKKVSFAHLHLAPSFGLHLSLKELDMHGIF  
 RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFFGLLYVDLSDNRISGAARPVAITREVDGRERVLPSR  
 NLAPRPLDTRLSEDFMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL  
 DLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMTQGVGHNL SFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC  
 10 ALDFSGNDLSRMWAEGLDLYLRFFQGLRSLVWLDLSQNLHTLLPRALDNLPSKSLKHLHLRDNLAFFNWSSTLL  
 PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPFGFALAKQLEELNLSANALKTVEPSWFGSMVGN  
 LKVL DV SANPLHCACGATFVGFLLEVQAAVPGLP SRVKCGSPGQLQHSIFAQDLRLCLDETL SWNCFGISLLAM  
 ALGLVVPMLHLCGWDLWYCFHLCLAWLPHRGQRGADALFYDAFVVDKAQSAVADWVYNELRVQLEERRGRRRA  
 LRLCLEERDWPGLKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQQRLLDRKDVVVLVILRPDAYRS  
 15 RYVRLRQRLCRQSVLLWPHQPRGQGSFQAQLGTALTRDNHFFYNRNFCRGPTTAE

## SEQ ID NO:6 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRLPAPFLPCELOPHGLVNCNWFLKSVPHFSAAAPRANVTSLSLLSNRIH  
 HLHDSDFVHLSSLRTLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS  
 20 RTNIVLVDPTHTLGLHALRYLYMDGNCYKNPCQGALEVVPGALLGLGNLTHLSLKYNLLEVPRLPPSLETLL  
 LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGLVLKDSLYNLDT  
 RWFRGLDRLQVLDLSENFLYDCITKTTFQGLARLRLSNLSFNHKKVSFAHLHLAPSFGLHLSLKELDMHGIF  
 RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFFGLLYVDLSDNRISGAARPVAITREVDGRERVLPSR  
 NLAPRPLDTRLSEDFMPNCKAFSFTLDLSRNNLVITIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL  
 25 DLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMTQGVGHNL SFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC  
 ALDFSGNDLSRMWAEGLDLYLRFFQGLRSLVWLDLSQNLHTLLPRALDNLPSKSLKHLHLRDNLAFFNWSSTLL  
 PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPFGFALAKQLEELNLSANALKTVEPSWFGSMVGN  
 LKVL DV SANPLHCACGATFVGFLLEVQAAVPGLP SRVKCGSPGQLQHSIFAQDLRLCLDETL SWNCFG

## 30 SEQ ID NO:7 (Porcine TLR9)

gagcacgaacatccttcactgtagctgctgcccggctctgccagccagaccctttggagaagacccccactccctgt  
 catgggcccccgctgcaccctgcacccctttctctcctggtgcaggtgacagcgctggctgcggctctggccca  
 gggcaggtgcctgccttcctgcctgtgagctccagcccaaggcctggtgaactgcaactggctctcctgaa  
 gtccgtgccccactctcctggcgagcgcggcccaagcgtcaccagcctcctcctactctcaaacgcatacca  
 35 ccacctgcacgactccgacttcgtccacctgtccagcctacgaactctcaacctcaagtggactgccgcggc  
 tggcctcagcccatgcacttccctgccacatgaccatcgagcccaacaccttctgcccgtgccaccctgga  
 ggagctgaacctgagctacaacagcatcacgaccgtgctgcccactccctcgtgtccctgtcgctgag  
 ccgcaccaacatcctggtgctagacccacccacctcactggcctacatgccctgcgctacctgtacatggatgg  
 caactgctactacaagaacccctgccagggggcgctggaggtggtgccgggtgccctcctcgccctgggcaacct  
 40 cacacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgct  
 gttgtcctacaaccacattgtcacccctgacgcctgaggacctggccaatctgactgccctgcgctgcttgatgt  
 gggggggaactgcgcgcgtgtgacatgcccgaacccctgcaggagtgcccaaaggaccaccccaagctgca  
 ctctgacaccttcagccacctgagccgcctcgaaggcctggtgttgaaagacagttctctctacaacctggacac  
 caggtggttccgaggcctggacaggtccaagtgtggacctgagtgagaacttctctacgactgcatcaccaa  
 45 gaccacggccttcaggggcctggcccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtcctt  
 tgccacactgcacctggcaccctcctttgggcacctccggtccctgaaggagctggacatgcatggcatcttctt  
 ccgctcgctcagtgagaccagctccaacctctgggtccaactgcctatgctccagaccctgcgctgcagatgaa  
 ctctaccaggccagctcagcatctttggggccttccctggcctgctgtacgtggacctatcggaacacgg  
 catcagcggagctgcaaggccagtgccattactagggaaggtggtgtagggagaggtctgtgctccttcacg  
 50 gaacctcgctccacgtccactggacactctccgctcagaggacttcatgcaaaactgcaaggccttcagcttcac  
 cttggaacctgtctcggaacaacctggtgacaatccagtcggagatgtttgctcgctctcacgcctcgagtgcct  
 gcgctgagccacaacagcatctcccaggcggtcaatggctctcagtttgctcgctgaccagcctgcgggtgct  
 ggacctgtcccacaacagctggacctgtatcacggcgctcggttcacggagctgcgcgctggaagcactgga  
 cctcagctacaatagccagccctttaccatgcagggtgtgggccacaacctcagcttcgtggccagctgcccgc

- 12 -

cctgcgctacctcagcctggcgacaaatgacatccatagccgagtggtcccagcagctctgtagcgcctcactgtg  
 cgccctggacttttagcgggcaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaagg  
 cctaagaagcctagtctggctggacctgtcccagaaccacctgcacacctcctgccacgtgccctggacaacct  
 ccccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcct  
 5 gcccagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcac  
 ccagctgaggagctggacctcagtggaacagcatcggtcttctgaacctggcttcttggcctggccaagca  
 gttagaagagctcaacctcagcgcgaatgccctcaagacagtggagccctcctgggttggctcgatgggtgggcaa  
 cctgaaagtccctagacgtgagcgccaacctctgcactgtgctgtggggcgaccttcgtgggttctctgtgga  
 ggtacaggctgacctgggtgggtgcccagcgcgtcaagtggtgagtcggggcgagctccaggcccatagcat  
 10 ctttgcgaagacctgcgctctgacctggtgagacctctcgtggaactgttttggcatctcgctgctggccat  
 ggccctgggctgggttgtgcccactgctgcaccacctctgcggctgggacctctggtactgcttccacctgtgct  
 ggctggctgccccaccgagggcagcggcgggcgagacgcctgttctatgatgccttcgtggtcttggacaa  
 agctcagagtgtgtggccgactgggtgtacaacgagctgagggtgcagctggaggagcgcctggcgccgcgc  
 actgcgctgtgctggaggagcagactggttacctggcaagacgtctctcgagaacctgtgggctcagtcta  
 15 cagcagccgcaagacctgttctgtgctggcccacacggacctgtcagcggcctcttgcgtgccagtcttctgt  
 ggccagcagcgcctgtggaggaccgcaaggacgttgtagtgtggtgatcctgcgcccagctccacgctc  
 ccgtacgtgagcgtgcgcccagcctctgcgcgagagtgctcctctctggccccaccagcccggtgggaggg  
 cagcttctgggcccagctgggacagccctgaccagggaacaaccaccacttctataaccggaacttctgcgggg  
 cccacgacagccgaatagcactgagtgcagccagctgtgcccagccccctggatttgcctctctgcctgggg  
 20 tgcccaacctgttctgctcagccacaccactgctctgctccctgttccccacccacccccagcctggcatgt  
 aacatgtgcccaataaatgctaccggaggggccaagaaaaaaaaaaaaaaaaa

## SEQ ID NO:8 (Porcine TLR9)

atggggccccgcgtgcacctgcaccccccttctctcctgggtgcaggtgacagcgcctggctgcccgtctggccag  
 25 ggcaggtgcctgccttctcgcctgtgagctccagccccacggcctgggtgaactgcaactggctcttctgaag  
 tccgtgccccacttctcgccggcagcgcggcgcccaacgtcaccagcctctccttactctccaaccgcatccac  
 cacctgcagcacttcgtccacctgtccgagcctacgaaactctcaacctcaagtggaaactgccgcggct  
 ggccctcagccccatgcacttcccctgccacatgacctcgagcccaacaccttctggccgtgccaccctggag  
 gagctgaacctgagctacaacagcatcacgacctgctgcccactccctcgtgctccctgtcgctgagc  
 30 cgcaccaacatcctggtgctagacccccaccacctactggcctacatgccctgcgctacctgtacatggatggc  
 aactgctactacaagaaccttgcagggggcgctggaggtggtgcccgggtgccctcctcgccctgggcaacct  
 acacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgtc  
 ttgtctacaaccattgtcacctgacgcctgaggacctggcgaatctgactgccctgcgctgcttcatgtg  
 ggggggaactgcccgcgtgtgacctgcccgaacctgcaggagtgcccaaggaccaccccaagctgcac  
 35 tctgacaccttcagccacctgagcgcctcgaaggcctgggtgtgaaagacagttctctctacaacctggacacc  
 aggtggttccgagggcctggacaggctccaagtgtgacctgagtgagaacttctctacgactgcatcaccaag  
 accagggccttccagggcctggcccagctgcgcagcctcaacctgtccttcaattaccacaagaagggtgtcctt  
 gccacctgcacctggcacctccttgggacacctcggtccctgaaggagctggacatgcatggcatcttctc  
 cgctcgctcagtgagaccagctccaacctctgggtccaactgcctatgctccagacctgcgctgcagatgaac  
 40 ttcatataaccaggcccagctcagcatcttggggccttccctggcctgctgtacgtggacctatcggaacaccg  
 atcagcggagctgcaaggccagtgccattactaggaggtggatggtagggagagggcttggtgcttccagg  
 aacctcgctccacgtccactggacactctccgctcagaggacttcagtcgcaaacgtgcaaggccttcagcttacc  
 ttggacctgtctcggaacaacctggtgacaatccagtcggagatgttctgctcgctctcacgctcgagtgcctg  
 cgctgagccacaacagcatctccaggcggtcaatggctctcagtttgtccgctgaccagcctgcccgtgctg  
 45 gacctgtcccacaacagctggacctgtatcacggcgctcggtcacggagctgcccgcctggaagcactggac  
 ctgagctacaatagccagccctttaccatgcagggtgtgggcccacaacctcagcttctggggccagctgcccgc  
 ctgctacctcagcctggcgacaaatgacatccatagccgagtggtcccagcagctctgtagcgcctcactgtg  
 gccctggactttagcggcaacgatctgagccgagtggtgggtgagggagacctctatctccgcttcttccaaggc  
 ctaagaagcctagtctggctggacctgtcccagaaccacctgcacacctcctgccacgtgccctggacaacctc  
 50 cccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcctg  
 cccaagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcacc  
 cagctgaggagctggacctcagtggaacagcatcggtcttctgaacctggcttcttggcctggccaagcag  
 ttagaagagctcaacctcagcgcgaatgccctcaagacagtggagccctcctgggttggctcgatgggtgggcaa  
 ctgaaagtccctagacgtgagcgccaacctctgcactgtgctgtggggcgaccttcgtgggttctctgctggag  
 55 gtacaggctgacctgggtgcccagcgcgtcaagtggtgagtcggggcgagctccaggcccatagcatc  
 ttgcgcaagacctgcgctctgacctggatgagacctctcgtggaactgttttggc

- 13 -

## SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPAPFLPCELPQHPGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
5 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCPRALEVAPGALLGLGNLTHLSLKYNNTLTPVPRRLPPLSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTSFHLRLEGLVLKDSLSLYKLEK  
DWFRGLGRQLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF  
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAPPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
GLAPGPLDAVSSKDFMPSCNLFNLTDLNRNLTITQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
10 LSHNKL DLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNL SFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL  
KILDVSANPLHCACGAADFVDFLLERQEA VPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFGLSLLMVA  
LGLAVPMLHHL CGWDLWYCFHLCLAHLP RRRRQRGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEERRGRRAL  
15 RLCLERD WLP GKTLFENLWASVYSSRKT MFVLDHTDRVSGLLRASFLLAQQRLLDRKDVVVLVILRPAAYRSR  
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGIALTRDNHRHFYNRNFCRGPTTAE

## SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPAPFLPCELPQHPGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
20 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCPRALEVAPGALLGLGNLTHLSLKYNNTLTPVPRRLPPLSLDTLL  
LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTSFHLRLEGLVLKDSLSLYKLEK  
DWFRGLGRQLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSFAHLHLASSFGSLVSLEKLDMHGIF  
RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAPPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR  
25 GLAPGPLDAVSSKDFMPSCNLFNLTDLNRNLTITQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD  
LSHNKL DLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNL SFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVLP  
RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVPGFFVRATRLIELNLSANALKTVDPSWFGSLAGTL  
KILDVSANPLHCACGAADFVDFLLERQEA VPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFG  
30

## SEQ ID NO:11 (Bovine TLR9)

gggaagtgggcccgaagcatccttccctgcagctgcctcccaacctgcccgcagaccctctggagaagccgcac  
tccctgtcatgggcccctactgtgccccgaccccccttctctcctggtgcaggcggcgccactggcagcgccc  
35 tggccgagggcaccctgctgccttccctgcccgtgagctccagcccatggtcagggtggactgcaactggctgt  
tcctgaagtctgtgccgcacttttcggctggagcccccgggccaatgtcaccagcctctccttaactctccaacc  
gcatccaccacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcc  
cgccggcggcctcagcccatgcaacttcccctgcgcatgaccatcgagcccaacaccttccctggtgtgccc  
ccctggaggagctgaacctgagctacaacggcatcacgacctgacctgacctgacctgacctgacctgacctg  
40 cgctgagccacaccagcatcctggtgctagggccccaccacttcaccggcctgcacgccccctgaccttctgtaca  
tggacggcaactgctactacatgaaccttgcggcgggccctggagggtggccccaggcgccctcctcgccctgg  
gcaacctcacgcacctgtcgctcaagtacaacaacctcacggagggtgccccgcgacctgccccccagcctggaca  
ccctgtgctgtcctacaaccacattgtcaccctggcaccggaggacctggccaacctgactgacctgacctg  
ttgacctgggtgggaactgcgcgcgtgcgacctgccccgaaccttgcaggagtgcccaagaaacttcccc  
agctgcaccttgacaccttcagtcacctgagccgctcgaaggcctggtgtgaaggacagttctctctacaaac  
45 tagaagaagattggttccgcgccctgggcaggctccaagtgcctgcacctgagtgaagaacttctctatgactaca  
tccaagaccacctcttcaacgacctgaccagctgcgagactcaacctgtccttcaattaccacaagaagg  
tgtccttcgcccacctgcacctagcgtcctccttgggagctcgtgtccttgagaagctggacatgcacggca  
tcttcttcgctccctcaccaacatcacgctccagtcgctgacctggctgccccagctccagagctctgcacatgc  
agctgaacttcatcaaccaggcccagctcagcatcttggggccttcccagacctgctctcgtggacctgtcgg  
50 acaaccgcatcagcggagccgcgacgcccagcggccctgggggaggtggacagcagggtggaagtctggcgat  
tgcccaggggcctcgctccaggcccgtggacgcccgtcagctcaaaggacttcatgccaagctgcaacctcaact  
tcaccttgacctgtcacggaacaacctggtgacaatccagcaagagatgtttaccgcctctcccgcctccagt  
gcctgcgctgagccacaacagcatctcgaggcggttaatggctcccagttcgtgcgctgaccagcctgcgag

- 14 -

tgctcgacctgtcccacaacaagctggacctgtaccatgggcgctcattcacggagctgccgcagctggaggcac  
tggacctcagctacaacagccagcccttcagcatgcaggcgctggggccacaacctcagcttcgtggccagctgc  
cctccctgcgtacctcagccttgccgacaaatggcatccacagccgctgtcacagaagctcagcagcgctcgt  
tgcgcgcccctggacttcagcggcaactccctgagccagatgtgggcccaggaggacctctatctctgctttttca  
5 aaggcttgaggaaacctgggtccagctggacctgtccgagaaccatctgcacaccctcctgcctcgtcacctggaca  
acctgcccagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgaccg  
tcttgcctccggttggagccctggatctggcaggaaaccagctgaaggccctgagcaacggcagcctgccgctg  
gcatccggctccagaagctggacgtgagcagcaacagcatcggttcgtgatccccggcttcttctgctccgcgcga  
ctcggtgatagagcttaacctcagcgccaatgccctgaagacagtggatccctcctgggttcggttcccttagcag  
10 ggacctgaaaatcctagacgtgagcgccaacctgcctccactgcctgcggggcgccctttgtggacttctgc  
tggagcagcaggagccgtgcccgggtgtccagcgcgctcacatgtggcagtcggggccagctccagggccgca  
gcatcttcacacaggacctgcgctctgcctggatgagacctctccttggactgctttggcctctcactgctaa  
tgggtggcgctgggctggcagtgcccatgctgcaccacctctgtggctgggacctctggctactgcttccacctgt  
gtctggccctttgcccagcggcgggcagcgggcgaggacacctgctctatgatgcgctcgtggctcttcg  
15 acaaggtgcagagtgcagtggtgattgggtgtacaacgagctccgctgcagctggaggagcgccggggggcgcc  
ggcgctccgctctgcctggaggagcgagactggctccctggtaagacgctcttcgagaacctgtgggctcgg  
tctacagcagccgcaagacctgttcgtgctggacacagcgaccgggtcagcgccctcctgcgcgaccttcc  
tgcctggccagcagcgtgttggaggaccgaagcagctcgtagtgtggtgatcctgcgccccgcgcctatc  
ggtcccgctacgtgcggtgcgcccagcgctctgcgcccagagcgtcctccttggccccaccagccagtggtcc  
20 agggtagtttctgggccaacctgggcatagccctgaccagggaacaacctcacttctataaccggaacttctgcc  
ggggccccacgacagccgaatagcacagagtgactgcccag

## SEQ ID NO:12 (Bovine TLR9)

atggggccctactgtgccccgcaccccttctctcctgggtgcaggcgggcgactggcagcgccctggccgag  
25 ggcacctgcctgccttctgcctgtgagctccagcccatgggtcaggtggactgcaactggctgttctctgaag  
tctgtgcccgaacttttcggtggagcccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac  
cacttgcatgacttgacttgcctccacctgtccaaacctgcgggtcctcaacctcaagtggaaactgccgcggcc  
ggcctcagccccatgcacttcccctgcggtatgacctcgagcccaacaccttctggctgtgcccacctggag  
30 gagctgaacctgagctacaacggcatcacgacctgcctgccctgccagttccctcgtgtccctgtcgtgagc  
cacaccagcatcctgggtgctaggccccaccacttcaccggcctgcacgcccctgcgcttctgtacatggacggc  
aactgctactacatgaacccctgcccgcgggcccctggaggtggccccaggcgccctcctcggcctgggcaacctc  
acgcacctgtcgtcaagtacaacaacctcacggaggtgccccgcgcgctgccccccagcctggacacctgctg  
ctgtctacaaccacattgtcaccctggcaccgaggaacctggccaacctgactgccctgcgctgcttgacgtg  
ggtgggaactgcccgcgctgcgacctgcccgaacctgcaggagtgcccaagaactccccaaagtgcac  
35 cctgacaccttcagtcacctgagccgctcgaaggcctgggtgtgaaggacagttctctctacaaactagagaaa  
gattgggtccgcggcctgggcaggctccaagtgtcgcacctgagtgagaacttctctatgactacatcaccaag  
accacctcttcaacgacctgacctgagctgcgagactcaacctgtccttcaattaccacaagaaggtgtccttc  
ggccacctgacctagcgtcctccttgggagctctgggtgtccctggagaagctggacatgcaggcatcttcttc  
cgctccctcaccaacatcacgctccagtcgctgacctggcctgcccagctccagagctctgcatctgcagctgaac  
40 ttcataaccaggcccagctcagcatcttggggccttcccagcctgctcttcgtggacctgtcggacaaccgc  
atcagcggagccgagccagcggccgcccctggggaggtggacagcagggtggaagtctggcgattgcccagg  
ggcctcgtctcaggcccgctggacggcctcagctcaaaggacttcagccaagctgcaacctcaacttcaccttg  
gacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcctctcccgcctccagtgctgcgc  
ctgagccacaacagcatctgcaggcggttaattggctcccagttcgtgcccgtgaccagcctgcgagtgctcgac  
45 ctgtcccacaacaagctggacctgtaccatgggcgctcattcacggagctgcccagctggaggcactggacctc  
agctacaacagccagcccttcagcatgcaggcggtggggccacaacctcagcttcgtggccagctgcctccctg  
cgctacctcagccttgccgacaaatggcatccacagccgctgtcacagaagctcagcagcgctcgttgccgccc  
ctggacttcagcggcaactccctgagccagatgtgggcccagggagacctctatctctgcttttcaaaggcttg  
aggaacctgggtccagctggacctgtccgagaacctctgcacacctcctgcctcgtcacctggacaacctgccc  
50 aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagctgacctcctgccc  
cggttggagccctggatctggcaggaaaccagctgaaggccctgagcaacggcagcctgccgctggcatccgg  
ctccagaagctggagctgagcagcaacagcatcggttcgtgatccccggcttcttcgtccgcgcgactcggtg  
atagagcttaacctcagcgccaatgccctgaagacagtggtatccctcctgggttcggttcttagcagggacctg  
aaaatcctagacgtgagcgccaacctgcctgcgctgcggggcgcccttctgtggacttctgctggagaga  
55 caggaggccgtgcccggtgtccaggcgctcacatgtggcagtcggggccagctccagggccgcagcatcttc  
acacaggacctgcgctctgcctggatgagacctctccttggactgctttggc



## SEQ ID NO:13 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPPLPCELQPHGLVNCNWLFLKSVPHFSAAPRDNVTSLSLLSNRI  
 HHLHDSDFQAQSLNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL  
 5 SRTNIIQLDPTSLTGLHALRFLYMDGNCYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTVPRSLPPSLEYL  
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN  
 PRWFRGLGNLTVDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFSGSLSLQELDMHGIF  
 FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQGLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS  
 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
 10 LDLSHNKLDDLYHGSRFTELPRLEALDLSYNSQPFMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
 WALDFSGNLSQMWAEGLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSSLTL  
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSNSII FVVPGFFALATRLRELNLSANALRTEEPSWFGFLAG  
 SLEVLVDVANPLHCACGAAFVDFLLQVQAAVPGLP SRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGLSLLV  
 VALGLAMPMLHHLGWDLYCFHLGLAWLPRRGWQRGADALSYDAFVVFDAQSAVADWVYNELRVRLREERRGR  
 15 ALRLCLEERDWPGLKTFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQQRLLDRKDVVVLVILSPDARR  
 SRYVRLRQLRQSVLFWPHQPSGQRSFQAQLGMALTRDNRHFYNQNF CRGPTMAE

## SEQ ID NO:14 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPPLPCELQPHGLVNCNWLFLKSVPHFSAAPRDNVTSLSLLSNRI  
 20 HHLHDSDFQAQSLNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLIL  
 SRTNIIQLDPTSLTGLHALRFLYMDGNCYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTVPRSLPPSLEYL  
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN  
 PRWFRGLGNLTVDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFSGSLSLQELDMHGIF  
 FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQGLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS  
 25 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV  
 LDLSHNKLDDLYHGSRFTELPRLEALDLSYNSQPFMRGVGHNLSFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL  
 WALDFSGNLSQMWAEGLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSSLTL  
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSNSII FVVPGFFALATRLRELNLSANALRTEEPSWFGFLAG  
 SLEVLVDVANPLHCACGAAFVDFLLQVQAAVPGLP SRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG

30

## SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgttgccgcgtgaagggactgcgagcacaaagcatcctcctctgagctgctgccagtg  
 tgccagctggaccctctggatcatctccactcctctgcatgggccccttgccatggtgccctgcagccctgtct  
 ctctggtgcaggcgccatgctggcgtggtctgcccgaaggcaccctgcctcccttctgcccgtgtgagctc  
 35 cagccccacggcctggtgaactgcaactggctgttctgaagtcctgccccacttctcagcagcagcaccggg  
 gacaatgtcaccagccttctctgtctccaaccgcatccaccacctccacgactccgactttgcccactgtcc  
 aacctgcagaaactcaacctcaaatggaactgccgcgacggcctcagccccatgcacttcccctgccacatg  
 accatcgagcccaacacttctctggtgtaccacccctggaggagctgaacctgagctacaacggcatcacgact  
 gtgcctgcccctgccagctccctctgtgtccctgatcctgagcgcaccaacatcctgcagctagacccaccagc  
 40 ctacgggctgcagctgcctgctctctatacatggatggcaactgctactacaagaacccctgcccggggcc  
 ctggaggtggccccaggcgccctccttgccctgggcaacctcaccacctgtcactcaagtacaacaacctcaca  
 acggtgccccgcagcctgccccctagcctggagctacgtgtgtgtctcctacaaccacattgtcaccctggcacct  
 gaggacctggccaatctgactgccctgctgtgtctgatgtgggtggaaactgccgcgctgtgacctgcacgc  
 aacctctgctggagtgccacataaatccccagctgcactccgacacctcagccacctaaagccgctagaa  
 45 ggctctgtgtgaaggatagttctctctaccagctgaacccagatggttcctggtggcctgggcaacctcacagt  
 ctgcactgagtgagaacttctctacgactcatcaccaaaacaaaggcattccagggcctggcccagctgcga  
 agactcaactgtccttcaattaccataagaaggtgtccttcgcccacctgacgctggcaccctccttcgggagc  
 ctgctctccctgcaggaaactggacatgcatggcatcttcttcgctcactcagccagaagacgctccagccactg  
 gcccgcctgcccagctccagcgtctgtatctgcagatgaacttcatcaaccaggcccagctcgccatcttcaag  
 50 gacttccctggtctgcgctacatagacctgtcagacaaccgcatcagtgaggctgtggagccggtggccaccaca  
 ggggaggtggatgggtgggaagaaggtctggctgacatccagggaacctcactccaggcccactggacacccccagc  
 tctgaggacttcatgccaagctgcaagaacctcagcttcccttgacctgtcacggaacaacctggtaacagtc  
 cagccagagatgtttgcccagctctcgcgcctccagtgctgcgcctgagccacaacagcatctcgaggcggtc

atgggcccttggccatgggtgcacctgagccctgtctctctcctgggtgcaggcgcccatgctggcggtggctctggcc  
caaggacccttgcctcccttccctgacctgtgagctccagccccacggcctgggtgaactgcaactggctgttccctg  
aagtccgtgccccacttctcagcagcagcaccgccgggacaatgtcaccagcctttccttgctctccaaccgcac  
30 caccacctccacgactccgactttgcccaactgtccaacctgcagaaactcaacctcaaagtgaactgcccgcca  
gccggcctcagccccatgacttccctgccacatgaccatcgagcccaactttcctggctgtaccaccctg  
gaggagctgaacctgagctacaacggcatcacgactgtgcctgccctgccagctcctcctgtgctcctgactgt  
agccgcaccaacatcctgcagctagacccccaccagcctcagggcctgcactgcctcgcttccatatacatggat  
ggcaactgtactacaagaacctgtcgggcgggcctggaggtggccccagggcgccctcctggcctgggcaac  
35 ctaccacctgtcactcaagtacaacaacctcacaacggtgccccgcagcctgccccctagcctggagtagcctg  
ctgttgcctacaaccacattgtcaccttggcacctgaggacctggccaatctgactgccctgcgtgtgctcgat  
gtgggtggaaactgccgcgctgtgaccatgcacgcaacctctgcgtggagtgcccacataaattccccagctg  
cactccgacaccttcagccacctaaagccgcttagaaggcctcgtgttgaggatagttctctctaccagctgaac  
cccagatggttcogtggcctgggcaacctcacagtgtctgacctgagtgagaacttctctacgactgcatcac  
40 aaaaccaaggcatccagggctggccactgctgcgaagactcaactgtctctcaattaccataagaagggtctcc  
ttcgccacctgacgtggcacctccttctgggagcctgtctccttgcaggaaactggacatgcatggcatcttc  
ttcgctcactcagccagaacgctccagcactggccccgctgcccatgtctccagcgtctgtatctgcagatg  
aacttcatcaaccaggccccagctcggcatcttcaaggacttccctggctgcgctacatagacctgtcagacaac  
cgcacagtgaggctgtggagccggtggccaccacaggggagtggtggtgggaagaaggctctggctgacatcc  
45 agggacctcactccaggccccactggacacccccagctctgaggacttcatgccaaagctgcaagaacctcagcttc  
accttggacctgtcacggaacaacctggtaacagtccagccagagatggttggccagctctcgccctccagtg  
ctgcgctgagccacaacagcatctcgaggcggtcaatggctcacagttcgtgcactgaccagcactgcagggt  
ctggacctgtcccaataacaaactggacctgacctgaggcgctcgtttacggagctgcgcgactggaggccctg  
gacctcagctacaacagcagcccttcagcatgcggggtgtggggccacaacctcagcttctgtggcccagctgcc  
50 accctgcgtacctcagcctggcacacaatggcatccacagccgtgtgtccagcagctctgcagcaacctcgctg  
tgggccctggacttcagcggcaattccctgagccagatgtgggctgaggagacctctatctccgcttcttccaa  
ggcctgagaagcctaattccggctagacctgtccagaatcgtctgcataacctcctgccatgcacctgggcaac  
ctccccaagagcttgcagctgtcgcgtctccgtaacaattacctggccttcttcaattggagcagcctgacctt  
ctgccccaaacctggaaacctggacctgggtggaaccagctgaaggctctgagcaatggcagcctgcttctggc  
55 acccagctccagaggctggagctcagcaggaacagcatcatcttctggtcctcctggcttcttctgctctggccacg  
aggctcgagagctcaacctcagtgccaacgccctcaggacagaggagccctcctgggttgggttctctagcaggc  
tcccttgaagctctagatgtgagcgccaacctctgcactgcgcctgtggggcagccttctgtggacttccctgctg

- 17 -

cagggttcaggctgccgtgcctggtctgccagccgctcaagtgtggcagtcggggccagctccaggccgcagc  
atcttcgcacaagacctgcgcctctgcctggacaagtcctctcctgggactgttttgg

## SEQ ID NO:17 (Ovine TLR9)

5 MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQQA VEAPGALLGLGNLTHLSLKYNNTLTPRRLPPLSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSLSLYKLEK  
10 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLQRLRLNLSFNHYHKKVSFAHLQLAPSFGGLVSLEKLDMHGIF  
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFVLDLSDNRISGAARPVAALGEVDSGVEVWRWPR  
GLAPGPLAAVSAKDFMPSCNLTLDLNRNLTITQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD  
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSLTVP  
15 QLEALDLAQNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFVLANRLKELNLSANALKTVPDFWFGRLTETL  
NILDVSANPLHCACGAAFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFGFSLLMVA  
LGLAVPMLHHLGWDLYCFHLCLAHLPRLRRRQGEDTLLYDAFVVFDAQSAVADWVYNELRVQLEERRGRRL  
RLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLEDKDVVVLVILRPAAYRSR  
YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGMALTRDNRHFYNRNFCRGPTTAE

## 20 SEQ ID NO:18 (Ovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTSLSLISNRIH  
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSSLVLSLS  
RTSILVLGPTHFTGLHALRFLYMDGNCYYKNPCQQA VEAPGALLGLGNLTHLSLKYNNTLTPRRLPPLSLDTLL  
LSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKNFPKLHPDTFSHLSRLEGLVLKDSLSLYKLEK  
25 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTLQRLRLNLSFNHYHKKVSFAHLQLAPSFGGLVSLEKLDMHGIF  
RSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFVLDLSDNRISGAARPVAALGEVDSGVEVWRWPR  
GLAPGPLAAVSAKDFMPSCNLTLDLNRNLTITQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD  
LSYNKLDLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLFSVAQLPSRLYLSLAHNGIHSRVSQKLSSASLRA  
LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSLTVP  
30 QLEALDLAQNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFVLANRLKELNLSANALKTVPDFWFGRLTETL  
NILDVSANPLHCACGAAFVDFLLEMQAAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFG

## SEQ ID NO:19 (Ovine TLR9)

gtcggcacgggaagtgcagcgccaagcatccttccctgcagctgccgcccacttgcccgcagaccctctggaga  
35 agccgcattccctgccatggggccctactgtgcccgcacccctttctctcctggtgcaggcgccggcgctggc  
agcagccctggcccagggcaccctgcctgccttctgcccgtgagctccagccccgggtaaggtgaactgcaa  
ctggctgttctgaagtctgtgcccgccttttcggccggagccccccgggcaatgtcaccagcctctcctta  
ctccaaccgcatccaccacttgacgactctgacttcgtccacctgtccaacctgcgggctctcaacctcaagt  
40 gaactgcccgcggccggcctcagccccatgcacttccctgcccgcagatgaccatcgagcccaacaccttctggc  
tgtgcccacctggaggagctgaacctgagctacaatggcatcacgaccgtgcctgcccctgcccagttctctcgt  
atccctgtcgctgagccgcaccagcatcctggtgctaggccccaccacttcaccggcctgcacgcctgcgctt  
tctgtacatggacggcaactgctactataagaacccctgccagcaggcctggaggtggccccaggcgccctcct  
tggcctgggcaacctcacgcacctgtcgtcaagtacaacacctcacggaggtgccccgcggcctgccccccag  
cctgggacacctgctgctgtcctacaaccacatcatcaccctggcaccgcaggacctggccaatctgactgcct  
45 gctgtgcttgatgtggcggggaactgccgcgctgcgaccacgcccgaacccctgcaggagtgcccaagaa  
cttccccaaagctgcacctgcacacttcagccacctgagccgcctcgaaggcctggtgtgaaggacagttctct  
ctacaaactagagaaagactgggtccgcggcctgggcaggctccaagtgtcgacctgagtgagaacttctcta  
tgactacatcaccaagaccacatcttcagggaacctgaccagctgcccagactcaacctgtccttcaattacca  
caagaaggtgtccttcgcccacctgcaactggcaccctcctttgggggcctggtgtcctggagaagctggacat  
50 gcacggcatcttcttcgctccctcaccaacaccacgctccggccgctgaccagctgcccagctccagagctt  
gagctgcagctgaacttcatcaaccaggccgagctcagcatctttggggccttcccagagcctgctcttcgtgga  
cctgtcggacaaccgcatcagcggagctgcgaggccggtggccgcctcggggaggtggacagcgggggtggaagt  
ctggcgggtggccaggggcctcgctccaggcccgctggccgcctcagcgcaaggaacttcatgccaagctgcaa

- 18 -

cctcaacttcaccttggaactgtcacggaacaacctggtagcatccagcaggagatgtttaccgcctctcccg  
cctccagtgcctgcgctgagccacaacagcatctcgcaggcggttaatggctcgcagttcgtgccgctgacccg  
cctgcgagtgctcgacctgtcctacaacaagctggacctgtaccatgggcgctcgttcacggagctgcgcgagct  
ggaggcactggacctcagctacaacagccagcccttcagcatgcagggcgctgggccacaacctcagcttcgtggc  
5 ctagctgccgtccctgcgctacctcagccttgccgacaaacggcatccacagccgctgtcacagaagctcagcag  
cgctcgtgcgcgccctggacttcagcggcaactccctgagccagatgtgggcgaggagacctctatctctg  
cttcttcaaaggcttgaggaacctggctccagctggacctgtccaagaaccacctgcacacctcctgcctcgtca  
cctggataacctgccaagagcctgcgcgagctgcgtctcgggacaataacctggccttcttcaactggagcag  
cctgactgttctgccccagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcct  
10 gccacctggcaccggctccagaagctggacgtgagcagcaacagcatcggtttgtgacctggcttcttctgt  
ccttgccaacggctgaaagagcttaacctcagcgccaaacgcctgaagacagtggatcccttctgggttcggtcg  
cttaacagagacctgaatatcctagacgtgagcgccaaacccgctccactgtgcctgcggggcgcccttctgtgga  
cttctcgtggagatgcaggcgccgctgcctgggctgtccaggcgctcacgtgtggcagtcggggccagctcca  
ggggccgagcatcttcgcacaggacctgcgcctctgcctggatgagacctctccttgactgctttggcttctc  
15 gctgctaattgggtggcgctgggctggcggtgccatgctgcaccacctctgtggctgggacctgtggtactgctt  
ccacctgtgtctgccccagctggaagccctggatctggcgggaaaccagctgaaggccctgagcaacggcagcct  
ggcttctgcacaaggcgagagtgagtgccgagctgtgtacaaacagctccgctgagcagtgaggagcgccg  
cgggcgccgggctccgctctgcctggaggagcgagactggctccctggcaagacgctcttcgagaacctgtg  
ggcctcggtctacagcagccgtaagaccatgttctgtgtggaccacacggaccgggtcagtgccctcctgcgcgc  
20 cagcttctcgtggccagcagcgctgttgaggaccgcaaggatgtcgtggtgctggatcctgcgccccgc  
cgctaccggctccgctacgtgcggctgcgccagcgctctgccgccagagcgctcctccttgccccaccagcc  
cagtgggccagggtagcttctgggccaacctgggcatggccctgaccagggaacccgaccttctataaccggaa  
cttctgcggggggcccaacagcagccgaatagcacagagtgaactgccag

## 25 SEQ ID NO:20 (Ovine TLR9)

atggggccctactgtgccccgcaccccttctctcctggtagcaggcgggcgctggcagcagccctggccag  
ggcaccctgcctgccttctgcctgtgagctccagcccggggtaagggtgaactgcaactggctgttctgaa  
tctgtgcgcgcttcttcggccggagcccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac  
30 cacttgcaagactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcccgccggcc  
ggcctcagccccatgcacttcccctgcgcagatgacctcgagcccaacaccttctggctgtgcccacctggag  
gagctgaacctgagctacaatggcatcacgacccgtgcctgcccagttctctcgtatccctgtcgtgagc  
cgccaccagcatcctgggtgctaggccccaccaccttcaccggcctgcacgcccctgcgcttctgtacatggacggc  
aactgtactataagaaccttgcagcaggccgtggaggtggccccaggcgccctccttgccctgggaacctc  
acgcacctgtcgtcaagtacaacaacctcagcgaggtgcccccgccctgccccccagcctggacacctgctg  
35 ctgtcctacaaccacatcatcaccctggcaccgaggacctggccaatctgactgccctgcgtgtgcttgatgtg  
ggcgggaaactgcccgccgtgcgaccacgcccgaaccttgcaggagtgcccaaagaacttccccaaagtgcac  
cctgacaccttcagccacctgagccgctcgaaggcctgggtgtgaaggacagttctctctacaaactagagaaa  
gactgggtccgcggcctgggcaggctcaaagtgtcgcacctgagtgagaacttctctatgactacatcaccaag  
accaccatcttcaggaacctgaccagctgcgcagactcaacctgtccttcaattaccacaagaagggtgtccttc  
40 gcccacctgcaactggcaccctccttgggggctgggtgcccctggagaagctggacatgcacggcatcttcttc  
cgctccctcaccaacaccagctccggccgctgaccagctgcccaagctccagagtctgagctctgcagctgaac  
ttcatcaaccaggccgagctcagcatcttggggccttcccagacctgctctcgtggacctgtcggaacaacgc  
atcagcgagctgcgagccgggtggccgcccctcggggaggtggacagcggggtggaagtctggcggtggccagg  
ggcctcgtccaggcccgctggccgcccctcagcgcaaggacttcatgccaagctgcaacctcaacttcaccttg  
45 gacctgtcacggaacaacctgggtgacgatccagcaggagatgtttaccgcctctcccgcctccagtgccctgcgc  
ctgagccacaacagcatctcgcaggcggttaatggctcgcagttcgtgcgctgaccgctcgtgcagtgctcgac  
ctgtcctacaacaagctggacctgtaccatggcgctcgttcacggagctgcgcgagctggaggcactggacctc  
agctacaacagcccttcagcatgcaggcgctgggcccacaaacctcagcttcgtggccagctgcccctcctg  
cgctacctcagccttgcgcacaacggcatccacagccgctgtcacagaagctcagcagcgctcgtgcgcgccc  
50 ctggacttcagcggaacctccctgagccagatgtggggccgaggagacctctatctcgttcttcaaaggcttg  
aggaaacctggctcagctggacctgtccaagaaccacctgcacacctcctgcctcgtcacctggataacctgccc  
aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgactgttctgccc  
cagctggaagccctggatctggcggaacccagctgaaggccctgagcaacggcagcctgcacctggcaccggg  
ctccagaagctggagctgagcagcaacagcatcggttctgtgacctggcttcttctgcttggcaaccggctg  
55 aaagagcttaacctcagcgccaacgcctgaagacagtggatcccttctgggtcggtcgcttaacagagacctg  
aatatcctagacgtgagcgccaacccgctccactgtgcctgcggggcgcccttctgtggactcctgctggagatg

- 19 -

caggcgccgtgcctgggctgtccaggcgcggtcacgtgtggcagtcggggccagctccaggggccgcagcatcttc  
gcacaggacctgcgctctgcctggatgagacctctccttggaactgctttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are  
publicly available. For example, an amino acid sequence for canine TLR9 is available as  
GenBank accession number BAC65192 and its corresponding nucleotide sequence is  
available as GenBank accession number AB104899. An amino acid sequence for feline  
TLR9 is available as GenBank accession number AAN15751 and its corresponding  
nucleotide sequence is available as GenBank accession number AY137581.

Complete nucleotide and amino acid sequences for canine and feline TLR9 were also  
determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on  
comparison with known amino acid sequences of human and murine TLR9, it appears that  
SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the  
transmembrane domain, and at least a portion of the intracellular domain of canine TLR9  
(See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively  
extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide  
sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides  
91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-  
822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on  
comparison with known amino acid sequences of human and murine TLR9, it appears that  
SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the  
transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See  
Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular  
domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline  
TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID  
NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID  
NO:25.

#### SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPALPCELPQHLVNCNWFLKSVPRFSAAAPRGNVTSLSLYSNRI  
HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSLVSLSL  
SRTNILLVLDPATLAGLYALRFLFDGNCYYKNPCQALQVAPGALLGLGNLTHLSLKYNNLTVVPRGLPPSLEYL

- 20 -

LLSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKGFQPLHPNTFGHLSHLEGLVLRDSSLYSLD  
 PRWFHGLGNLMVLDLSENFLYDCITKTAFYGLARLRRLNLSFNHKKVSFAHLHLASSFGSLLSLQELDIHGIF  
 FRSLSKTTTLQSLAHLPMQLRLHLQNLFIQAQLSIFGAFPLRYVDLSDNRISGAAPAAATGEVEADCGERVWP  
 5 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVPQEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
 RVLDSLHNKLDLYHGRSFTLPRLEALDLSYNSQPFMRGVGHNLFSVAQLPALRYLSLAHNGIHSRVSQQLRSA  
 SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRHLTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL  
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSPFFALAVRLRELNLNLSANALKTVEPSWFGSL  
 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSVCFSL  
 LAVALSLAVPMLHQLCCGWDLWYCFHLCLAWLPRRGRRRGVDALAYDAFVVFDAQSSVADWVYNELRVQLEERRG  
 10 RRALRLCLEERDWPVGKTLFENLWASVYSSRKTLFVLARTDRVSGLLRASFLAQQRLLDRKDVVVLVILCPDA  
 HRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNHRHFYNQNFRCGPPTA

## SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLVQAAALALALAQGTLPALPCELPQPHGLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI  
 15 HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCMTIEPNTFLAVPTLEDNLNSYNSITVPALPSSLVSLSL  
 SRTNIVLDPATLAGLYALRFLFLDGNICYKNPCQQALQVAPGALLGLGNLTHLSLKYNNTLVVPRGLPPSLEYL  
 LLSYNHIITLAPEDLANLTALRVLDVGGNCRCDHARNPCRECPKGFQPLHPNTFGHLSHLEGLVLRDSSLYSLD  
 PRWFHGLGNLMVLDLSENFLYDCITKTAFYGLARLRRLNLSFNHKKVSFAHLHLASSFGSLLSLQELDIHGIF  
 20 FRSLSKTTTLQSLAHLPMQLRLHLQNLFIQAQLSIFGAFPLRYVDLSDNRISGAAPAAATGEVEADCGERVWP  
 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVPQEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL  
 RVLDSLHNKLDLYHGRSFTLPRLEALDLSYNSQPFMRGVGHNLFSVAQLPALRYLSLAHNGIHSRVSQQLRSA  
 SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRHLTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL  
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSPFFALAVRLRELNLNLSANALKTVEPSWFGSL  
 25 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGLPSPRVKCGSPGQLQGRSIFAQDLRLCLDEALSWSVCF

## SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaagcatcctttcctgcagctgctgcccagcctgccagccagaccctctggagaag  
 cccccgctccctgtcatgggccccctgccgtggcgccctgcacccccctgtctctcctggtgcaggtgcgcgceta  
 gcccctggccctggcccagggcaccctgccttccctgcctgtgagctccagcccatggcctggtgaactgc  
 30 aactggctgttccctcaagtcgctgccccgcttctcggcagctgcaccccgcggaacgtcacagcctttccttg  
 tactccaaccgcatccaccacctccatgactatgactttgtccacttcgtccacctgcggcgtctcaatctcaag  
 tggaaactgcccgcggccagcctcagcccatgcactttccctgtcacatgaccattgagcccaacaccttccctg  
 gctgtgcccaccctagaggacctgaatctgagctataacagcatcacgactgtgcccgccttgcaggttcgctt  
 gtgtccctgtccctgagcgcaccaaactcctggtgctggaccctgccaccctggcaggcctttatgccctgccc  
 35 ttccctgttccctggaatggcaactgctactacaagaacccctgccagcaggccctgcaggtggccccaggtgcctc  
 ctggcgctgggcacactcacacactgtcactcaagtaacaacacccctcacctggtgcccgcgggctgcccc  
 agcctggagtaactgctcctgtcctcacacacatcatcaccctggcactgaggacctggcaatctgactgcc  
 ctgctgtcctcgatgtgggtgggaactgtcgccgctgtgacctgcccgttaacccctgcaggagtgcccaag  
 ggcttccccagctgcaccccaacaccttcggccacctgagccacctcgaaggcctggtgttgaggagacagctct  
 40 ctctacagcctggacccaggtggttccatggcctgggaacctcatggtgctggacctgagtgagaacttccctg  
 tatgactgcatcaccaaaacaaagccttctacggcctggcccggtgcgcagactcaacctgtccttcaattat  
 cataagaaggtgtcctttgccacctgcatctggcatcctccttcgggagcctactgtccctgcaggagctggac  
 atacatggcatcttctccgctcgctcagcaagaccagctccagtcgctggccacctgcccagctgctccagcgt  
 ctgcatctgcagttgaactttatcagccaggccagctcagcatcttcggcgcccttccctggactgcggtacgtg  
 45 gacttgtcagacaaccgcatcagtgagctgcagagcccgcggtgccacagggaggtagaggcagactgtggg  
 gagagagtctggccacagctcccggaacttgcctctgggcccactgggcaaccccggtcagaggccttcatgccg  
 agctgcaggacctcaacttcaccttgacctgtctcggaacaacctagtactgttcagccggagatgtttgtc  
 cggtggcgccctccagtgctggcctggcctgagccacaacagcatctcgaggcggtcaatggctgcagttcgtg  
 cctctgagcaacctgcgggtgctggacctgtccataaagctggacctgtaccacgggcgctcgttcacggag  
 50 ctgcccgcggctggaggccttgacctcagctacaacagccagccctcagcatgcggggcggtgggcccacatctc  
 agctttgtggcagctgcagcctgcgctcagctcagcctggcgcaaatggcatccacagccgctgtcccag  
 cagctccgcagcgctcgtccgggccccctgactcagtgggcaataacctgagccagatgtgggcccagagagac  
 ctctatctccgcttcttccaaggcctgagaagcctggttcagctggacctgtccagaatcgccctgcataccctc  
 ctgccacgcaacctggacaacctcccaagagcctgcggctcctgcggctccgtgacaattacctggctttcttc  
 55 aactggagcagcctggccctcctacccaagctggaagccctggacctggcgggaaaccagctgaaggccctgagc

- 21 -

aatggcagcttgcccaacggcaccagctccagaggctggacctcagcggcaacagcatcggcttcgtgggtccc  
 agcttttttgccttgccgtgaggttcgagagctcaacctcagcgccaacgccctcaagacggtggagccctcc  
 tggtttggttccctggcggtgacctgaaagtccctagacgtgaccgccaaccccttgcatcgtctgctggcgca  
 accttcgtggacttcttgcagggtgaggtgcgggtgcccggcctgcctagccgtgtcaagtgcggcagcccg  
 5 ggccagctccaggggcgagcatcttcgcacaggacctgcgcctctgcctggacgaagcgtctcctgggtctgt  
 ttcagcctctcgtgctggtgctggtgacctgagcctggctgtgcccattgctgcaccagctctgtggctgggacctc  
 tggtaactgcttccacctgtgacctggcctggctgccccggcgggggcgggcggtgtggatgacctggcctat  
 gacgccttcgtggtcttcgacaaggcgagagctcgggtggcgactgggtgtacaatgagctgcgggtacagcta  
 gaggagcgctggcgcgggcgctacgcctgtgtctggaggaaagctgactgggtaccggcaaaacctcttc  
 10 gagaacctctgggacctcagtttacagcagccgcaagacgtgtttgtgctggcccgacggacagagtcagcggc  
 ctctgctgctgagcttctgctggcccaacagcgctgctggaggaccgcaaggacgtcgtggtgctggtgatc  
 ctgtgccccgacgcccacgctcccgtatgtgctggctgcgcagcgctctgcgcagagctcctcctctggt  
 cccaccagccagtggtgacgagcgttctgggcccagctgggacggccctgaccagggacaacggccacttc  
 tacaaccagaacttctgcggggggccacgacgctgtaggcagacagccagcacttcgcgcccctacacc  
 15 ctgctgtctgctgggatgcccagactgctggctctacaccgcgctctgtctcccctacaccagccctggca  
 taaagcgaccgctcaataaatgctgctggttagac

## SEQ ID NO:24 (Canine TLR9)

atggggccctgcccgtggcgccctgcacccctgtctctcctgggtgcaggtgcgcgctagccctggccctggcc  
 20 cagggcacctgacctgaccttctgacctgtgagctccagcccatggcctggtgaactgcaactggtgttctc  
 aagtcgctgccccgttctcggcagctgcaccccgcggttaacgtcaccagccttctctgtactccaaccgcatc  
 caccacctccatgactatgactttgtccacttcgtccacctgcggcgctctcaatctcaagtggaaactgcccggcc  
 gccagcctcagcccatgcaacttccctgtcacatgaccattgagcccaacaccttccctggctgtgcccacccta  
 gaggacctgaatctgagctataacagcatcacgactgtgcccgcctgcccagttcgttgttccctgtccctg  
 25 agccgcaccaacatctcgggtgctggacctgcccacctggcagcctttatgacctgccttctgttccctggat  
 ggcaactgctactacaagaacccctgccagcagggcctgcaggtggccccaggtgacctcctggcggtggcaac  
 ctcacacacctgtcactcaagtaacaacacctcacgtggtgcccggggcctgccccccagcctggagtacctg  
 ctcttgtcctacaaccacatcatcacctggcacctgaggacctggccaatctgactgacctgctgctcctgat  
 gtgggtgggaactgtcgccgctgtgacctgcccgttaacccctgcagggagtgcccaagggtctccccagctg  
 30 caccccaacaccttcggccacctgagccacctcgaaggcctggtgttgaggagacagctctctctacagcctggac  
 ccaggtggttccatggcctgggcaacctcatggtgctggacctgagtgagaacttccctgtatgactgcatcacc  
 aaaaccagaaccttctacggccttctcggcctgcccagctcgaacctgtccttcaattatcaagaagggtgtcc  
 ttgcccacctgcatctggcatcctccttcgggagcctactgtccctgcaggagctggacatacatggcatcttc  
 ttccgctcgtcagcaagaccagctccagtcgctggccccacctgcccattgctccagcgtctgcatctgcagttg  
 35 aactttatcagccaggcccagctcagcatcttcggcgcttccctggactgcggtacgtggacttgtcagacaac  
 cgcacagtgaggctgcagagcccgcgctgccacaggggaggttagaggcagactgtggggagagagctctggcca  
 cagtcccggaaccttgcctctgggcccactgggacccccggctcagaggccttcatgccagctgcaggacctc  
 aacttcaccttggaacctgtctcggaacaacctagtgttgcagccggagatgtttgtcgggtggcgcgctc  
 cagtgcctgggctgagccacaacagcatctcgaggcggtcaatggctcgcagttcgtgctctgagcaacctg  
 40 cgggtgctggacctgtcccataaacaagctggacctgtaccacggcgctcgttcacggagctgcccgggctggag  
 gccttggacctcagctacaacagccagcccttcagcatgcggggcggtgggcccacaatctcagcttctgtggcacag  
 ctggcagccctgcgtacctcagcctggcgcaaatggcatccacagccgctgtcccagcagctccgcagcgcc  
 tcgctccggggccctggacttcagtggaataacctgagccagatgtggggcagggagacctctatctccgcttc  
 ttccaaggcctgagaagcctggttcagctggacctgtcccagaatcgctgcataacctcctgccacgcaacctg  
 45 gacaacctccccaaagcctgcggtcctgcggctcctgtgacaattacctggcttcttcaactggagcagcctg  
 gccctcctacccaagctggaagccttgacctggcgggaaaccagctgaaggcctgagcaatggcagcttgccc  
 aacggcaccagctccagaggctggacctcagcggaacagcatcggcttcgtggtccccagcttttttgcctg  
 gccgtgaggtctcgagagctcaacctcagcgccaacgccctcaagacggtggagccctcctggtttggttccctg  
 50 gcgggtgacctgaaagtccctagacgtgaccgccaaccccttgcatcgtctgcggcgcaaccttcgtggacttc  
 ttgctggagggtgcaggtgcgggtgcccggcctgcctagccgtgtcaagtgcggcagcccgggcagctccagggc  
 cgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgtctcctgggtctgtttcagc

## SEQ ID NO:25 (Feline TLR9)

MGPCGHALHPLSLLVQAAALAVALAQGTLPAPFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLSYNSRI  
 55 HHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITVPALPSSLVLSLSL

- 22 -

SRTNIVLVD PANLAGLHSLRFLFDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSLNHLLEGLVLKDSSLYNLN  
 PRWFHALGNLMVLDLSENFLYDCITKTAFQGLAQLRRRLNLSFNHKKVSAHLHLAPSFGLSLSLQQLDMHGIF  
 FRSLSETTLRSLVHLPMLQSLHLQMFNINQAQLSIFGAPFGLRYVDLSDNRISGAMELAAATGEVDGGERVRLPS  
 5 GDALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMSQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRHLTLPRTLDNLPKSLRLLRLRDNYLAFFNWSSSLVL  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG  
 TLKVL DVTGNPLHCACGA AFVDFLEVQA AVPGLP GHVKCSPGQLQGRSIFAQDLRLCLDEALS WDCFGLSLT  
 10 VALGLAVPMLHHL CGWDLWYCFHLCLAWLPRRGRRGADALPYDAFVFDKAQSAVADWVYNELRVRL EERRGR  
 ALRLCLEERDWPGLKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQRLLLED RKDVVVLVILRPDAHR  
 SRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNF CRGPTTAE

## SEQ ID NO:26 (Feline TLR9)

15 MGPCHGALHPLSLVLVQAAALAVALAQGTLP AFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTLSLSYSNRI  
 HHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCMTIEPHTFLAVPTLEELNLSYNSITVPALPSSLSVLSL  
 SRTNIVLVD PANLAGLHSLRFLFDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL  
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSLNHLLEGLVLKDSSLYNLN  
 20 PRWFHALGNLMVLDLSENFLYDCITKTAFQGLAQLRRRLNLSFNHKKVSAHLHLAPSFGLSLSLQQLDMHGIF  
 FRSLSETTLRSLVHLPMLQSLHLQMFNINQAQLSIFGAPFGLRYVDLSDNRISGAMELAAATGEVDGGERVRLPS  
 GDALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQV  
 LDLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMSQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL  
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRHLTLPRTLDNLPKSLRLLRLRDNYLAFFNWSSSLVL  
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG  
 25 TLKVL DVTGNPLHCACGA AFVDFLEVQA AVPGLP GHVKCSPGQLQGRSIFAQDLRLCLDEALS WDCFG

## SEQ ID NO:27 (Feline TLR9)

aggggtctgcgagctccaggcattctctctgcccctgcctgcccagctctgccatccagaccctctggagaagcccc  
 cactccctgtcatgggcccctgccatggcgccctgcacccctgtctctcctgggtgcaggtgcccgcctggccg  
 30 tggccctggcccaggcaccctgcctctctgcccctgtgagctccagcgccacggcctggtagattgcgact  
 ggctgttccctcaagtccgtgccccactctctcgccggcagcgccccgtggtaacgtcaccagccttccctgtact  
 ccaaccgcatccaccacctccagcactccgactttgtccacctgtccagcctgcccgcctctcaacctcaaatgga  
 actgcccacccgcccagcctcagccccatgcacttccctgtcacatgaccattgagccccacaccttccctggccg  
 tgcccacccctggaggagctgaacctgagctacaacagcatcacgacagtaccgcccctgccaggttccctcgtgt  
 35 cctgtccttgagccgtaccaacatcctgggtgctggaccctgccaacctcgcagggctgcactccctgcgcttct  
 tgctcctggatggcaactgctactacaagaacccctgcccgaggccctgcaggtggccccggggcgccctccttg  
 gcctgggcaaccttacgcacctgtcactcaagtacaacaacctcactgcggtgccccgcggcctgccccccagcc  
 tggagtacctgtattgtcctacaaccacatcatccctggcactgaggacctggccaacctgaccgcctgc  
 gtgtgctcgatgtgggtgggaactgccgtcgctgtgaccacgcccgaacccctgtatggagtggcccaagggct  
 40 tcccgacactgcaccctgacaccttcagccacctgaaccacctcgaaggcctgggtgtgaaggacagctctctct  
 acaacctgaaccccagatgggtccatgcccctgggcaacctcatggtgctggacctgagtgagaacttccatata  
 actgcataccaaaaccacagccttccagggcctggcccagctgcgcagactcaacttgtcttcaattaccaca  
 agaaggtgtcctttgccacctgcactgtggcgccctccttcgggagcctgctctccctgcagcagctggacatgc  
 atggcactcttctccgctcgctcagcgagaccagcctccggtcgctgggtccacctgccatgctccagagctgc  
 45 acctgcagatgaacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacc  
 tgtcagacaaccgcataagtggagccatggagctggcggtgccacgggggaggtggatgggtggggagagagtcc  
 ggctgccatctggggacctagctctggggccaccgggacccttagctccgagggttcatgccaggctgcaaga  
 ccctcaacttcacctggacctgtcacggaacaacctagtgaacatccagccagagatggttggccggctctcgc  
 gcctccagtgctgctcctgagccgcaacagcatctcgacggcagtcacaggctcacaatttatgccgctgacca  
 50 gcctgcaggtgctggacctgtcccataacaagctggacctgtaccatggcgctctttcacggagctgccgcggc  
 tggaggccctggacctcagctacaacagccagcccttcagcatgcaggcggtgggtcacaacctcagcttctgtgg  
 cacagctgccggccctgcgctatctcagcctggcgcaacagacatccacagcgtgtgtcccagcagctgtga  
 gcgcctcgctggcggttggacttcagcggaatgccttgagccgatgtggggccgaggagacctgtatctcc  
 acttctccgaggcctgaggagcctgggtccggttgatctgtcccagaatcgctgcataccctcttgcacgca  
 55 ccctggacaacctcccaagagcctgcggctgctgcgtctccgtgacaattatctggcttcttcaactggagca



- 23 -

gcctggctcctcctccccaggetggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagct  
 tgcctaattggaaccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagcttttttg  
 ctctggccaccaggtgcgagagctcaacctcagtgccaacgccctcaagacggtggagccctcctgggttcggtt  
 5 ctctagcgggacacctgaaagtcctagatgtgactggcaacccctgcaactgcgctgtggggcggccttcgtgg  
 acttcttgctggaggtgcaggctgcagtgcccggcctgccaggccacgtcaagtgtggcagtcagggtcagctcc  
 agggccgcagcatctttgcgcaggatctgcgcctctgcttgatgaggccctctcctgggactgttttggcctct  
 cgctgctgaccgtggccctggcctggcctgcccctgctgcaccacctctgtggctgggacctctgggtactgct  
 tccacctgtgctggcctggctgcccggcgggggcgccgagggcgcgatgcccctgcccctacgatgcctttg  
 10 tggctctcgacaaggcacagagcgcggtggcgactgggtgtacaacgagctgcgggtacggctagaggagcgcc  
 gtggacggcgagcgctccgctgtgctggaggaaacgtgactggctaccgggtaaaacgctctttgagaacctgt  
 gggcctcagtttacagcagccgcaagatgctgtttgtgctggccacacagacagggtcagcggcctcttgccg  
 ccagctttctgctggccagcagcgctgctggaggaccgcaaggacgtgtggtgctgggtgacctgcgccccg  
 acgcccaccgctcccgtatgtgcggctgcgcagcgctctgcgcagagcgctcctcctctggccccaccagc  
 ccagtggccagcgagcttctgggcccagctgggcacggccctgaccagggaacaccagcacttctataaccaga  
 15 acttctgcccggggccccacgacggcagagtgaccggccagcaccaccaagcctcctacacctgacctgtgctgctg  
 ggatgcccggg

## SEQ ID NO:28 (Feline TLR9)

atgggcccctgccatggcgccctgcacccctgtctctcctgggtgcaggctgcgcgctggcctggcctggcc  
 20 cagggcaccctgctgcctttctgccctgtgagctccagcgccacggcctgggtgaattgcgactggctgttcctc  
 aagtccgtgcccacttctcgggcgagcgccccgtggaacgtcaccagcctttccctgtactccaaccgcac  
 caccacctccagactccgactttgtccacctgtccagcctgcccgtctcaacctcaaatggaactgccaccc  
 gccagcctcagccccatgcacttcccctgtcacatgaccattgagccccacaccttccctggcgtgccacccctg  
 25 gaggagctgaacctgagctacaacagcatcacgacagtaccgccttcccaggttccctcgctgcccctgtccttg  
 agcgtaccaacatcctgggtgctggaccctgccacctcgagggctgcaactcctgctgttctgttctggat  
 ggcaactgctactacaagaaccttgcgcgagccctgcagggtggcccgcccgcccttggcctgggcaac  
 cttacgcacctgtcactcaagtacaacaacctcactgcgggtgccccgcggcctgccccccagcctggagtacctg  
 ctattgtcctacaaccacatcatcaccctggcacctgaggacctggccaacctgaccgcctcgctgtgctcgat  
 30 gtgggtgggaactgcgctgctgtgaccacgcccgaacccctgtatggagtggcccaagggttcccgcacctg  
 caccctgacaccttcagccacctgaaccacctcgaaggcctgggtgttgaggagacagctctctacaacctgaac  
 ccagatgggttccctggcctgggaacctcatgggtgctggacctgagtgaagaacttctatatgactgcatcacc  
 aaaaccacaccttccagggcctggccagctgcgcagctcaacttctttcaattaccacaagaagggtgtcc  
 35 tttgccacctgcatctggcgccctccttcgggagcctgctctccctgcagcagctggacatggcatcttct  
 tccgctcgctcagcgagaccagctccggctgctgggtccacctgcccctgctccagagctcgcacctgcagatg  
 aacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacctgtcagacaac  
 cgcataagtggagccatggagctggcggtgcccagggggaggtggatgggtggggagagagtccggctgccatct  
 40 ggggacctagctctggggccaccgggcacccctagctccgagggcttcatgccaggctgcaagacctcaacttc  
 accttggacctgtcacggaacaacctagtgaacatccagccagagatgtttgcccggtctcgcgctccagtg  
 ctgctcctgagccgcaacagcatctcgaggcagtcacaggtcacaatttatgccgctgaccagcctgcagggtg  
 ctggacctgtcccataacaagctggacctgtaccatggggcgtcttccagggagctgcccggctggaggccctg  
 45 gacctcagctacaacagccagcccttcagcatgcaggcggtgggtcacaacctcagcttctgggcacagctgccc  
 gccctgcgctatctcagcctggcgcaacacagatccacagccgtgtgtcccagcagctctgcagcgctcgctg  
 cgggccttggacttcagcggcaatgccttgagccggatgtggggcgaggagacctgtatctccacttctccga  
 ggctgaggagcctgggtccggttggatctgtcccagaatcgccctgcataacctcttgccacgcacctggacaac  
 50 ctccccaggctggaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagcttgccaatgga  
 accagctccagaggtggacctcagcagcaacagtatcagcttcgtggcctccagctttttgtctctggccacc  
 aggtgcgagagctcaacctcagtgccaacgccctcaagacggtggagccctcctgggttcgggtctctagcggg  
 acctgaaagtccatagatgtgactggcaacccctgcaactgcgctgtggggcgcccttcgtggacttctgtgctg  
 gaggtgcaggctgcagtgccggcctgccaggccacgtcaagtgtggcagtcagggtcagctccaggggccgcagc  
 atctttgcgcaggatctgcgctctgctggatgaggccctcctcctgggactgttttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide  
 5 sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide  
 10 sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

#### SEQ ID NO:29 (Murine TLR9)

MVLRRTTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI  
 15 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSSL  
 SHTNILLVDANSLAGLYSLRVLFMDGNCYKPNCTGAVKVTGALLGLSNLTHLSLKYNNTKVPRQLPPSLEYL  
 LVSYNLIVKLGPEDLANLTSRLVLDVGGNCRCDHAPNPCI ECGQKSLHLHPETFHHLSHLEGLVLKDSLSLHTLN  
 SSWFQGLVNLVLDLSENFLYESINHTNAFQNLTRLRKLNL SFNYRKKVS FARLHLASSFKNLVSLQELNMNGIF  
 20 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSNRI SGPSTLSEATPEEADDAEQEELL  
 SADPHAPLSTPASKNFMDCRCKNFKFTMDLSRNNLVITIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ  
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKGIHNF SFVAHLSMLHSLSLAHNDI HTRVSSHLSNSNS  
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL  
 25 FLPNLEVL DLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVD RSWFGPIV  
 MNLTVLDVRSNPLHCACGA FVDLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGLSLL  
 AVAVGMVVPILHHL CGWDVWYCFHLC LAWLPLLARSRRSAQALPYDAFVVDKAQSAVADWVYNELRVRL EERRG  
 RRALRLCLEDRDWLP GQTLFENLWASIYGSRKTLFVLAHTDRVSGLLRTSFLLAQORLLED RDKDVVVLVILRPDA  
 HRSRYVRLRQLRCRQSVLFWPQQPNGQGFWAQLSTALTRDNRHFYNQNFRCRGPTAE

#### SEQ ID NO:30 (Murine TLR9)

MVLRRTTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI  
 30 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCHMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSSL  
 SHTNILLVDANSLAGLYSLRVLFMDGNCYKPNCTGAVKVTGALLGLSNLTHLSLKYNNTKVPRQLPPSLEYL  
 LVSYNLIVKLGPEDLANLTSRLVLDVGGNCRCDHAPNPCI ECGQKSLHLHPETFHHLSHLEGLVLKDSLSLHTLN  
 SSWFQGLVNLVLDLSENFLYESINHTNAFQNLTRLRKLNL SFNYRKKVS FARLHLASSFKNLVSLQELNMNGIF  
 35 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSNRI SGPSTLSEATPEEADDAEQEELL  
 SADPHAPLSTPASKNFMDCRCKNFKFTMDLSRNNLVITIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ  
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFMSKGIHNF SFVAHLSMLHSLSLAHNDI HTRVSSHLSNSNS  
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL  
 40 FLPNLEVL DLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVPAFFALAVELKEVNLSHNILKTVD RSWFGPIV  
 MNLTVLDVRSNPLHCACGA FVDLLLEVQTKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

#### SEQ ID NO:31 (Murine TLR9)

tgtcagagggagcctcgggagaatcctccatctcccaacatgggttctccgtcgaaggactctgcaccccttgctcc  
 ctctggttacaggctgcagtgcgtggctgagactctggccctgggtaccctgcctgccttccctaccctgtgagctg

- 25 -

aagcctcatggcctgggtggactgcaattggctgttctctgaagtctgtaccccggttctctgcggcagcatcctgc  
 tccaacatcaccgcctctccttgatctccaaccgtatccaccacctgcacaactccgacttcgtccacctgtcc  
 aacctgcggcagctgaacctcaagtgggaactgtccaccactggccttagccccctgacttctcttgccacatg  
 accattgagccagaaccttctctggctatgctgacactggaggagctgaacctgagctataatgggtatcaccact  
 5 gtgccccgactgccagctccctgggtgaatctgagcctgagccacaccaatcctgggtctagatgctaacagc  
 ctgcgcggcctatacagcctgcgcgttctcttcatggacgggaactgctactacaagaaccttgcacaggagcg  
 gtgaaggtgaccccgagcgccctcctgggcctgagcaatctcaccatctgtctctgaagtataacaacctcaca  
 aagggtccccgcaactgccccccagcctggagctacctcctgggtgctataacctcattgtcaagctggggcct  
 gaagacctggccaatctgacctcccttcgagctacttgatgtgggtgggaattgcccgtcgctgcgacctgcccc  
 10 aatccctgtatagaatgtggccaaaagtccctccacctgcaccctgagaccttccatcacctgagccatctggaa  
 ggcctgggtgctgaaggacagctctctccatacactgaactcttctctgggttccaaggtctgggtcaacctctcggtg  
 ctggacctaaagcgagaacttctctatgaaagcatcaaccacaccaatgccttccagaacctaacccgcctgcgc  
 aagctcaacctgtccttcaattaccgcaagaaggtatccttggccgcctccacctggcaagtcccttcaagaac  
 ctgggtgctcactgcaggagctgaacatgaacggcatcttctccgctcgctcaacaagtacacgctcagatggctg  
 15 gccagctcgcccaactccacactctgcactcttcaatgaacttcatcaaccaggcacagctcagcatcttgggt  
 accttccgagcccttcgcttctgtggacttctcagacaaatcgcatcagtgggccttcaacgctgcgacctgcccc  
 cctgaagaggcagatgatgcagagcaggaggagctgtgtctgcggatcctcaccagctccactgagcaccct  
 gcttctaagaacttcatggacaggtgtaagaacttcaagttcaccatggacctgtctcggaacaacctgggtgact  
 atcaagccagagatgttctgtcaatctctcagcctcagtgcttagcctgagccacaactccattgcacaggct  
 20 gtcaatggctctcagttcctgcgcgtgactaatctgcaggtgctggacctgtcccataacaacctggacttgtac  
 cactggaaatcgctcagtgagctaccacagttgcaggccctggacctgagctacaacagccagcccttagcatg  
 aagggtataggccacaatttctcagtttctgtggccatctgtccatgtcacacagccttagcctggcacacaatgac  
 attcatacccggtgtgtcctcacatctcaacagcaactcagtgaggttcttgacttcagcggaacgggtatgggc  
 cgcatgtgggatgaggggggccttctatctccatttcttccaaggcctgagtggcctgctgaagctggacctgtct  
 25 caaaataacctgcatactcctccggccccagaaaccttgacaacctccccaaagagcctgaagctgctgagcctccga  
 gacaactacctatcttctttaaactggaccagctctgtccttctgcccacctggaagctcctagacctggcaggc  
 aaccagctaaaggccctgaccaatggcaccctgcctaatggcaccctcctccagaaactggatgtcagcagcaac  
 agtatcgtctctgtgggtcccagccttcttctgctctggcggtcgagctgaaagaggtcaacctcagccacaacatt  
 tcaagacgggtggatcgctcctgggttggggccattgtgatgaacctgacagttctagacgtgagaagcaacct  
 30 ctgcactgtcctgtggggcagccttcgtagacttactgttgaggtgcagaccaaggtgctggcctggccta  
 ggtgtgaagtgtggcagccccggccagctgcaggccgtagcatcttcgcacaggacctgcgctgtgacctggat  
 gaggtcctctcttgggactgcttggccttctactcttggtgtggcctgggcatgggtgctatactgcac  
 catctctgcgcgtgggacgtctggtactgttttcatctgtgctggcatggctaccttctgtggcccgagccga  
 cgcagcgcccaagctctccctatgatgccttctgtgttgataaaggcacagagcgagttgaggactgggtg  
 35 tataacgagctgcggtgcggtgaggagcgcgcggtgcgcgagccctacgcttgtgtctggaggaccgagat  
 tggctgctggccagacgtcttcgagaacctctgggcttccatctatgggagcgcaagactctatttgtgctg  
 gccacacggcagcgctcagtgccctcctgcgacacagcttctgctggtcagcagcgctgttggaagaccgc  
 aaggacgtgggtgtgtggtgacctgcgtccggtgcccacgcctccgctatgtgagcactgcgacgctctc  
 tgccgcagagtggtctcttctggccccagcagcccaacgggcaggggggttctggggccagctgagtacagcc  
 40 ctgactagggacaaccgaccttctataaccagaactctgcccgggacctacagcagaatagctcagagcaaca  
 gctggaaacagctgcatcttcatgcctgggttcccagagttgctctgcctgc

## SEQ ID NO:31 (Murine TLR9)

atgggttctccgtcgaaggactctgcaccccttgtccctcctggtagaggtgcagtgctgggtgagactctggcc  
 45 ctgggtaccctgcctgccttctaccctgtgagctgaagcctcatggcctgggtggactgcaattggctgttctg  
 aagtctgtaccccggttctctgcggcagcatcctgtctccaacatcaccgcctctccttgatctccaaccgtatc  
 caccacctgcacaactccgacttcgtccacctgtccaacctgcggcagctgaacctcaagtggaaactgtccaccc  
 actggccttagccccctgacttctcttgccacatgaccattgagccagaaacttctgggtatgctacactg  
 gaggagctgaacctgagctataatgggtatcaccactgtgccccgactgccagctccctgggtgaatctgagctg  
 50 agccacaccaacatcctgggtctagatgctaacagcctgcgcggcctatacagcctgcgcgttctcttcatggac  
 gggaaactgctactacaagaaccttgcacaggagcggtgaaggtgaccccgagcgccctcctgggcctgagcaat  
 ctacccatctgtctctgaagtataacaacctcacaaggtgccccgcaactgccccagcctggagtacctc  
 ctgggtgctctataacctcattgtcaagctggggcctgaagacctggccaatctgacctcccttcgagctacttgat  
 gtgggtgggaattgcccgtcgctgcgacctgcccccaatcctctgtatagaatgtggccaaaagtccctccacctg  
 55 caccctgagaccttccatcacctgagccatctggaagcctgggtgctgaaggacagctctctccatacactgaac  
 tcttctgggttccaaggtctgggtcaacctctcggtgctggacctaaagcgagaacttctctatgaaagcatcaac  
 cacaccaatgccttccagaacctaacccgcctgcgcaagctcaacctgtccttcaattaccgcaagaaggtatcc

- 26 -

tttgcccgcctccacctggcaagttccttcaagaacctgggtgctcactgcaggagctgaacatgaacggcatcttc  
 tccgctcgctcaacaagtacacgctcagatggctggccgatctgcccaactccacactctgcatcttcaaatg  
 aacttcatcaaccaggcacagctcagcatctttggtaccttccgagcccttcgctttgtggacttgtcagacaat  
 cgcatcagtgggccttcaacgctgtcagaagccaccctgaagaggcagatgatgcagagcaggaggagctgttg  
 5 tctgcggtatcctcaccagctccactgagcaccctgcttctaagaacttcatggacaggtgtaagaacttcaag  
 ttcacatggacctgtctcggaacaacctgggtgactatcaagccagagatgtttgtcaatctctcacgcctccag  
 tgtcttagcctgagccacaactccattgcacaggctgtcaatggctctcagttcctgcccgtgactaatctgcag  
 gtgctggacctgtcccataacaaactggacttgtaccactggaaatcggtcagtgagctaccacagttgcaggcc  
 ctggacctgagctacaacagccagccctttagcatgaagggtataggccacaatttcagttttgtggcccatctg  
 10 tccatgctacacagccttagcctggcacacaatgacattcatacccggtgtgtcctcacatctcaacagcaactca  
 gtgaggtttcttgacttcagcggcaacgggtatgggcccgtatgtgggatgagggggccctttatctccatttcttc  
 caaggcctgagtggtgctgtaagctggacctgtctcaaaataacctgcatactctccgccccagaaccttgac  
 aacctccccaagagcctgaagctgctgagcctccgagacaactacctatcttctttaactggaccagtctgtcc  
 ttcctgcccacctggaagtctagacctggcaggcaaccagctaaagggcctgaccaatggcaccctgcctaat  
 15 ggcaccctctccagaaactggatgtcagcagcaacagtatcgctctctgtggtcccagccttcttcgctctggcg  
 gtgcagctgaaagaggtcaacctcagccacaacattctcaagacgggtggatcgctctgtgttggggccattgtg  
 atgaacctgacagttctagacgtgagaagcaacctctgcactgtgctgtggggcagccttcgtagacttatg  
 ttggaggtgcagaccaaggtgcctggcctggctaattggtgtgaagtgtggcagccccggccagctgcaggccgt  
 agcatcttcgcacaggacctgcggctgtgcctggatgaggtcctctcttgggactgctttggc

20

## SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI  
 HHLHDSDFAHLP SLRHLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
 SHTNIMLDSASLAGLHALRFLFMDGNCYYKNPCQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL  
 25 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRCDHAPNPMCPCPRHFPQLHPDTFSLSRLEGLVLKDSLSLWLN  
 ASWFRGLGNLRVLDLSENFLYKCTTKTAFQGLTQLRKLNLNLSFNQKRVSAHLSLAPSFGLVALKELDMHGIF  
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSNRI SGASELTATMGADGGEKVWLQ  
 GD LAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
 LDLSRNKLDLYHEHSFTLPRLEALDLSYNSQPFQMVGHNFSFVAHLRTLRLSLAHNNIHSQVSQQLCSTSL  
 30 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLTLLPQTLRNLPKSLQVLRRLDNYLAFFKWWSLHF  
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDSWFGPLAS  
 ALQILDVSANPLHCACGAAMDFLLEVQAAVPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFA  
 VALGLGVPMLHHL CGWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVFDKTS AVADWVYNELRGQLEBCRG  
 RWALRLCLEERDWLP GKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDKDVVVLVILSPDG  
 35 RRSRYVRLRQLRCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFFYNRNFCQGPTAE

## SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRI  
 HHLHDSDFAHLP SLRHLNLKWNCPVGLSPMHFPCMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL  
 40 SHTNIMLDSASLAGLHALRFLFMDGNCYYKNPCQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYL  
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRCDHAPNPMCPCPRHFPQLHPDTFSLSRLEGLVLKDSLSLWLN  
 ASWFRGLGNLRVLDLSENFLYKCTTKTAFQGLTQLRKLNLNLSFNQKRVSAHLSLAPSFGLVALKELDMHGIF  
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSNRI SGASELTATMGADGGEKVWLQ  
 GD LAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV  
 45 LDLSRNKLDLYHEHSFTLPRLEALDLSYNSQPFQMVGHNFSFVAHLRTLRLSLAHNNIHSQVSQQLCSTSL  
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLTLLPQTLRNLPKSLQVLRRLDNYLAFFKWWSLHF  
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDSWFGPLAS  
 ALQILDVSANPLHCACGAAMDFLLEVQAAVPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFA

## 50 SEQ ID NO:35 (Human TLR9)

aggctgggtataaaaatcttacttctctattctctgagccgctgctgcccctgtgggaagggacctcgagtgtga  
 agcatccttccctgtagctgctgtccagctctgcccgcagacctctggagaagccctgccccccagcatgggt  
 ttctgcccgcagcgcctgcaccgctgtctctcctggtgcaggccatcatgctggccatgacctggccctgggt

- 27 -

accttgccctgccttccctaccctgtgagctccagccccacggcctggggaactgcaactggctgttccctgaagtct  
 gtgccccacttctccatggcagcaccctgggcaatgtcaccagccttccctgtcctccaaccgcatccaccac  
 ctccatgattctgactttgcccacctgcccagcctgcccgcctcctcaacctcaagtggaaactgcccgcgggtggc  
 5 ctgagccccatgcacttccccctgccacatgaccatcgagcccagcacttcttggtgtgcccaccctggaagag  
 ctaaacctgagctacaacaacatcatgactgtgcctgcgctgcccacaaatccctcatatccctgtccctcagccat  
 accaaccatcctgatgctagactctgcccagcctgcgcgctgcctgcgcttccctattcatggacggcaac  
 tgttattacaagaacccctgcaggcaggcactggagggtggccccgggtgcctccttggtggtgggcaacctcacc  
 cacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctgctgttg  
 10 tccataaacgcgcatcgctcaaacggcgctgaggacctggccaatctgaccgcccctgcgtgtgctcgatgtgggc  
 ggaaattgcccgcgctgcgaccacgctcccaaccctgcctggagtgccctcgctcacttccccagctacatccc  
 gataccttcagccacctgagccgtcttgaaggcctgggtgttgaaggacagttctctctcctgggtgaatgccagt  
 tgggtccgtgggtgggaaacctccgagtgctggacctgagtgagaacttccctctacaaatgcatcactaaaacc  
 aaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattacaaaagaggggtgtcctttgccc  
 15 cactgtctctgccccttccctcgggagcctggctgcctgaaggagctggacatgcacggcgccttcttccgc  
 tcaactcgatgagaccacgctccggccactggccgcctgcccctgctccagactctgcgtctgcagatgaacttc  
 atcaaccaggcccagctcggcatcttccagggccttccctggcctgcgctacgtggacctgtcggaacaaccgcac  
 agcggagcttccgagctgacagccaccatgggggagggagatggaggggagaaggtctggctgcagcctggggac  
 cttgctccgccccagtgagcactcccagctctgaagacttcaggcccaactgcagcaccctcaacttcaccttg  
 20 gatctgtcacggaacaacctggtagccgtgcagccggagatgtttgcccagctctcgcacctgcagtgccctgcgc  
 ctgagccacaactgcctctcgcaggcagctcaatggctcccagttctcgtccgctgaccggtctgcaggtgtctagac  
 ctgtcccgaataaagctggacctctaccacgagcactcattcacggagctaccgcgactggagcccttcttccgtc  
 agctacaacagccagcccttggcatgcaggcgctggggccacaacttcagcttctggtggtcactgcgcacctg  
 25 cggcacctcagcctggcccacaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgctgcggggcc  
 ctggacttcagcggcaatgcactggggccatgtgtggccgagggagacctctatctgcacttcttccaaggcctg  
 agcgggttgatctggtggactgtcccagaaccgctgcacaccctcctgccccaaacctgcgcaacctcccc  
 aagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtgggtggagcctccacttccctgccc  
 aaactggaagtccctgcacctggcaggaaaccggctgaaggccctgaccaatggcagcctgcctgctggcaccgg  
 30 ctccggaggctggatgtcagctgcaacagcatcagcttctgctggccccggcttcttttccaaggccaaggagctg  
 cgagagctcaaccttagcgccaacgcctcgaagacagctggaccactcctgggttggggccctgctggcagtgccctg  
 caaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgcccttcttgacttccctgctggaggtg  
 caggctgcctgcccgggtgctcccagccgggtgaagtgtggcagtcggggccagctccaggccctcagcatcttt  
 35 gcacaggacctgcgcctctgcctggatgaggccctctcctgggactgttccgcccctctcgctgctgggtgtggct  
 ctgggcctgggtgtgcccctgctgcctcacctctgtggctgggacctctgggtactgcttccacctgtgcctggcc  
 tggcttccctggcgggggcggaagtggcgagatgaggatgccttgcctacgatgccttctggtgtcttcgac  
 40 aaaacgcagagcgcagtgaggagactgggtgtacaacagacttccggggcagctggaggagtgcctggggcgctgg  
 gcactccgctgtgcctggagggaacgcgactgctgcctggcaaaacctcttggagaacctgtgggcctcggtc  
 tatggcagccgcaagacgctgtttgtgctggcccacaggaaccgggtcagtggtctcttgcgcgcagcttccctg  
 ctggcccagcagcgcctgctggaggaccgcaaggacgtcggtgtgctggatcctgagccctgacggccgcccgc  
 tcccgcctacgtgcggctgcgcccagcgcctctgcgcagagtgctcctcctctggcccaccagcccagtggtcag  
 45 cgcagcttctggggccagctgggcatggccctgaccaggggacaaccaccacttctataaccggaacttctgccag  
 ggaccacggccgaatagccgtgagccggaatcctgcacggtgccacctccacactcacctcacctctgcctgcc  
 tggctgacctccctgctgcctcctcaccacacactgacacagagca

## SEQ ID NO:36 (Human TLR9)

45 atgggtttctgcccagcgcctgcaaccgctgtctctcctgggtgcaggccatcatgctggccatgacctggcc  
 ctgggtaccttgccctgccttccctaccctgtgagctccagccccacggcctggggaactgcaactggctgttccctg  
 aagtctgtgccccacttctccatggcagcaccctgggcaatgtcaccagccttccctgtcctccaaccgcatc  
 caccacctccatgattctgactttgcccacctgcccagcctgcccgcctcctcaacctcaagtggaaactgcccgcgg  
 50 gttggcctcagccccatgcacttccccctgccacatgaccatcgagcccagcacttcttggtgtgcccaccctg  
 gaagagctaaacctgagctacaacaacatcatgactgtgcctgcgctgcccacaaatccctcatatccctgtccctc  
 agccataccaacatcctgatgctagactctgccagcctgcgcggcctgcctgcctgccttccctattcatggac  
 ggcaactgttattacaagaacccctgcaggcaggcactggagggtggccccgggtgcctccttgccctgggcaac  
 ctcaaccacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctg  
 55 ctggttccctacaaccgcctcgtcaaacctggcgctgaggacctggccaatctgaccgcccctgcgtgtgctcgat  
 gtggggggaattgcccgcgctgcgaccacgctcccaaccctgcctggagtgccctcgctcacttccccagcta  
 catcccgataccttcagccacctgagccgtcttgaaggcctgggtgttgaaggacagttctctctcctgggtgaat  
 gccagttgggtccgtgggctgggaaacctccgagtgctggacctgagtgagaacttccctctacaaatgcatcact

- 28 -

aaaaccaaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattaccaaagaggggtgtcc  
 ttgtccacactgtctctggcccttctcctcgaggcctggctgcctgaaggagctggacatgcacggcatcttc  
 ttccgctcactcgatgagaccagctccggccactggcccgctgccatgctccagactctgctgtcgcagatg  
 aacttcatcaaccagggccagctcggcactcttcagggccttccctggcctgcgctacgtggacctgtcggacaac  
 5 cgcatcagcggagcttcggagctgacagccaccatgggggagggagatggaggggagaaggtctggctgcagcct  
 ggggaccttgtctccggccccagtggaactcccagctctgaagacttcaggcccaactgcagaccctcaacttc  
 accttggatctgtcacggaacaacctggtgacctgacgagcgagatgtttgccagctctcgcacctgcagtgc  
 ctgcgctgagccacaactgcatctcgcaggcagtcattggctcccagttcctgcccgtgaccggtctgcaggtg  
 10 ctgacctgtcccgcataaagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctg  
 gacctcagctacaacagccagccctttggcatgcaggcgctggggccacaacttcagcttcgtggcctcacctgcgc  
 acctgcgccacctcagcctggcccacaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgtg  
 cgggacctggaacttcagcggcaatgcactggggccatatgtggggcgaggagacctctatctgcacttcttccaa  
 ggctgagcggtttgatctggctggactgtcccagaaccgcctgcacacctcctgccccaaacctgcgcaac  
 15 ctccccaaagagcctacaggtgctgctcctcgtagacaattacctggccttctttaagtggaggcctccacttc  
 ctgccccaaactggaagtccctgcacctggcaggaaccggctgaaggccctgaccaatggcagcctgcctgctggc  
 accggctccggaggtggatgtcagctgcaacagcatcagcttcgtggccccggcttcttttccaaggccaag  
 gagctgcgagagctcaaccttagcgccaacgcctcagaacagtgaggaccactcctgggttggccctggcagtg  
 gcctgcaataactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttatggacttctgctg  
 20 gaggtgcaggctgccgtgccggctgtcccagcgggtgaagtgtggcagtcggggccagctccagggcctcagc  
 atctttgcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgcc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9  
 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and  
 nucleic acid molecules encoding them are provided by the invention. The chimeric  
 25 polypeptides include at least one amino acid substitution based on a comparison of  
 conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine,  
 equine, ovine, canine, feline, and human TLR9. The information contained in a multiple  
 sequence alignment of these various TLR9 polypeptide sequences, provided for example in  
 Figure 1, can be used to identify and select individual amino acid positions and even  
 30 individual amino acids to substitute in designing a chimeric TLR9. The substitution or  
 substitutions can be effected using methods known to those of ordinary skill in molecular  
 biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be  
 inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino  
 35 acid for a second amino acid, wherein side chains of the first amino acid and the second  
 amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to  
 alter conformation. For example, conservative amino acid substitutions generally may be  
 made between members within each of the following groups: hydrophobic (A, I, L, M, V),  
 neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-  
 40 conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide  
5 sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked. With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is  
10 operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase,  $\beta$ -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in  
15 eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art.  
20 The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

25 In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid  
30 coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

- 30 -

Generally a nucleic acid coding sequence and a gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A “TLR9 ligand” as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA



- 31 -

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

5 The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine  
10 dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:

15 
$$5'-N_1X_1CGX_2N_2-3'$$

wherein  $X_1$  and  $X_2$  are nucleotides, N is any nucleotide, and  $N_1$  and  $N_2$  are nucleic acid sequences composed of from about 0-25 N's each. In some embodiments  $X_1$  is adenine, guanine, or thymine and/or  $X_2$  is cytosine, adenine, or thymine. In other embodiments  $X_1$  is cytosine and/or  $X_2$  is guanine.

20 Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a  
25 non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising  
30 a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

- 32 -

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

- 33 -

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the  $\beta$ -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease). Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

- 34 -

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has  
5 been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.  
10 Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by  
15 reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs,  
20 such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

25 Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid  
30 phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.

- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty  
 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene  
 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180  
 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000)  
 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and  
 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

	MBD-1	R-XXXXXXX-R-X-D-X-Y-XXXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
	hTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
	mTLR9	Q-XXXXXXX-K-X-D-X-Y-XXXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5	hTLR9	Q-VLDLSRN-K-L-D-L-Y-HEHSFTelp-R-L-EALDLS-Y	SEQ ID NO:68
	mTLR9	Q-VLDLSHN-K-L-D-L-Y-HWKSFSelp-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test  
15 compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of  
20 inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory nucleic acids. The immunostimulatory compound can be, for example, a nucleic acid  
25 molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or lipopolysaccharide, a small molecule.

A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a  
30 species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

- 37 -

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact  
5 with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a  
10 TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to  
15 immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving  
20 MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including  $\kappa$ B kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF- $\kappa$ B. Examples of such promoters include, without limitation, those for NF- $\kappa$ B, IL-1 $\beta$ , IL-6, IL-8, IL-12 p40, CD80,  
25 CD86, and TNF- $\alpha$ . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase,  $\beta$ -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- $\alpha$ ). In  
30 certain embodiments the reporter is selected from IL-8, TNF- $\alpha$ , NF- $\kappa$ B-luciferase (NF- $\kappa$ B-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

- 38 -

*Mol Cell Biol* 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF- $\kappa$ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of quantitative measurements of responses in each instance.

In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, I $\kappa$ B, NF- $\kappa$ B, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for screening species selectivity with respect to a given nucleic acid sequence.

Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test



- 39 -

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

### Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

*Cells and Tissues.* Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNeasy<sup>TM</sup> (Ambion<sup>®</sup>, Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

*First-strand cDNA synthesis.* Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzol™ reagent (GIBCO BRL®, Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using  
5 SUPERScript™ II reverse transcriptase (GIBCO BRL®, Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T<sub>(18)</sub>]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at  
10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl<sub>2</sub>) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERScript™ II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:  
20 forward primer 5'-ACCTTGCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38).

The 2.7 Kbp fragment was PCR amplified using Advantage® 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix  
25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

*Cloning and sequencing.* The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min  
30 at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZerO™ - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment  
5 were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

10 Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

*Results.* Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19,  
15 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

#### Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

20 Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, [www.cmbi.kun.nl/bioinf/tools/clustalw.shtml](http://www.cmbi.kun.nl/bioinf/tools/clustalw.shtml)). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple  
25 sequence alignment are presented in Figure 1. As will be appreciated from Figure 1, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, Figure 1 also indicates that certain amino  
30 acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

Figure 2 presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

### Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Since NF- $\kappa$ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- $\kappa$ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- $\kappa$ B-luciferase reporter plasmid (NF- $\kappa$ B-luc) or with hTLR9 alone. After stimulus with CpG-ODN (2006, 2 $\mu$ M, TCGTCGTTTGTGCTTTTGTGCTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 $\mu$ M, TGCTGCTTTTGTGCTTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- $\kappa$ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 $\mu$ M; TCCATGACGTTTCCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 $\mu$ M;

- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- $\kappa$ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- $\kappa$ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates ( $2 \times 10^6$  cells/plate) with 16  $\mu$ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- $\kappa$ B-luciferase activity after stimulation with  
10 ODN. Four different types of clones were generated.

293-hTLR9-luc:	expressing human TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-mTLR9-luc:	expressing murine TLR9 and 6-fold NF- $\kappa$ B-luciferase reporter
293-hTLR9:	expressing human TLR9
15 293-mTLR9:	expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20  $3 \times 10^6$  293T cells were electroporated with 5  $\mu$ g NF- $\kappa$ B-luc plasmid and 5  $\mu$ g of either horse TLR9-pcDNA3.1 plasmid or humanTLR9-pcDNA3.1 plasmid at 200V, 975  $\mu$ F. After the electroporation the cells were plated in 96-well cell culture plates at  $2.5 \times 10^4$  cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and  
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in Figure 3.

As shown in Figure 3, ODN 2006 (TCGTCGTTTTGTCGTTTTGTCGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982  
30 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

### Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

- 46 -

**Claims**

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

5. A vector comprising the nucleic acid of any of claims 3-4.

6. A cell comprising the vector of claim 5.

7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.

8. A method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:  
aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;  
generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the



- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with  
5 the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a  
15 CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the  
20 initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25

10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred  
30 CpG DNA).

- 48 -

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.

5           12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

10           14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:  
15           contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;  
              measuring a signal in response to the contacting; and  
              identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

20           17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

25           18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

30           20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- $\kappa$ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

20	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
25	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
30	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
35	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),
	TCCATGACGTCTTTGATGTT	(SEQ ID NO:55),
	TCCATGACGTATTTGATGTT	(SEQ ID NO:56), and
	TCCATGACGTGTTTGATGTT	(SEQ ID NO:57).

Figure 1  
(1/3)

```

feline      MGPCHGALHPLSLLVQAAALAVALAAGTLPAPFLPCELPQHGVLVNCNWLFLKSVPHFSAAA 60
canine      MGPCRGALHPLSLLVQAAALALALAAGTLPAPFLPCELPQHGVLVNCNWLFLKSVPRFSAAA 60
bovine      MGP-YCAPHPLSLLVQAAALAAALAEGLTLPAPFLPCELPQHGQVDCNWLFLKSVPHFSAGA 59
mouse       MGP-YCAPHPLSLLVQAAALAAALAEGLTLPAPFLPCELPQHGQVDCNWLFLKSVPHFSAGA 59
ovine       MGP-YCAPHPLSLLVQAAALAAALAEGLTLPAPFLPCELPQHGQVDCNWLFLKSVPHFSAGA 59
porcine     MGP-RCTLHPLSLLVQVTAALAAALAEGLTLPAPFLPCELPQHGVLVNCNWLFLKSVPHFSAAA 59
horse       MGPCGHALQPLSLLVQAAMLAVALAAGTLPAPFLPCELPQHGVLVNCNWLFLKSVPHFSAAA 60
human       MGFCRSALHPLSLLVQAIMLAMTLAGTLPAPFLPCELPQHGVLVNCNWLFLKSVPHFSMAA 60
rat         MVLCRRTLHPLSLLVQAALAEALALGTLAPFLPCELPKPHGLVDCNWLFLKSVPHFSAAE 60
*           : :*****. ** : * * *.***** : * * :*****: ** .

feline      PRGNVTSLSLYSNRIHHLHDSDFVHLSLRLNLKWNCPASLSPMHFPCHMTIEPHTFL 120
canine      PRGNVTSLSLYSNRIHHLHDYDFVHFVHLRLNLKWNCPASLSPMHFPCHMTIEPHTFL 120
bovine      PRANVTSLSLISNRIHHLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFL 119
mouse       PRANVTSLSLISNRIHHLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFL 119
ovine       PRANVTSLSLISNRIHHLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFL 119
porcine     PRANVTSLSLISNRIHHLHDSDFVHLSLRLNLKWNCPAGLSPMHFPCHMTIEPNTFL 119
horse       PRDNVTSLSLISNRIHHLHDSDFVHLSLRLNLKWNCPAGLSPMHFPCHMTIEPNTFL 120
human       PRGNVTSLSLSSNRIHHLHDSDFVHLSLRLNLKWNCPVGLSPMHFPCHMTIEPSTFL 120
rat         PRSNITSLSLIANRIHHLHNLDFVHLPNVRQLNLKWNCPPLGLSPLHFSRCMTIEPKTFL 120
** * :***** :*****: ** : : :***** .***:*. :***** **

feline      AVPTLEELNLSYNSITTVPALPSSVLVSLSRTNIIVLDPANLAGLSLRFELDGNCCYY 180
canine      AVPTLEDNLSYNSITTVPALPSSVLVSLSRTNIIVLDPATLAGLYALRFLFDGNCCYY 180
bovine      AVPTLEELNLSYNGITTVPALPSSVLVSLSRTNIIVLGPTHFTGLHALRFLYMDGNCCYY 179
mouse       AVPTLEELNLSYNGITTVPALPSSVLVSLSRTNIIVLGPTHFTGLHALRFLYMDGNCCYY 179
ovine       AVPTLEELNLSYNGITTVPALPSSVLVSLSRTNIIVLGPTHFTGLHALRFLYMDGNCCYY 179
porcine     AVPTLEELNLSYNSITTVPALPDSVLVSLSRTNIIVLDPHTLGLHALRFLYMDGNCCYY 179
horse       AVPTLEELNLSYNGITTVPALPDSVLVSLSRTNIIQLDPTSLTGLHALRFLYMDGNCCYY 180
human       AVPTLEELNLSYNNIMTVPALPKSLISLSHTNIIIMLDSASLAGLHALRFLMDGNCCYY 180
rat         AMRMLEELNLSYNGITTVPRLPSSLTNLSHTNIIVLDASSLAGLSLRLVFMDCGNCCYY 180
* : ** :*****. * *** ** . * ** : * * * . : : * : * * :*****

feline      KNPCQALQVAPGALLGLGNLTHLSLKYNLTAVPRGLPSPSLEYLLLSYNHIITLAPEDL 240
canine      KNPCQALQVAPGALLGLGNLTHLSLKYNLTVPRGLPSPSLEYLLLSYNHIITLAPEDL 240
bovine      MNPCPRALEVAPGALLGLGNLTHLSLKYNLTVPRRLPPLSDTLTLLSYNHIITLAPEDL 239
mouse       MNPCPRALEVAPGALLGLGNLTHLSLKYNLTVPRRLPPLSDTLTLLSYNHIITLAPEDL 239
ovine       KNPCQALEVAPGALLGLGNLTHLSLKYNLTVPRRLPPLSDTLTLLSYNHIITLAPEDL 239
porcine     KNPCQALEVAPGALLGLGNLTHLSLKYNLTVPRSLPSPSLEYLLLSYNHIITLAPEDL 239
horse       KNPCGRALEVAPGALLGLGNLTHLSLKYNLTVPRSLPSPSLEYLLLSYNHIITLAPEDL 240
human       KNPCQALEVAPGALLGLGNLTHLSLKYNLTVPRNLPSPSLEYLLLSYNRIIVKLAPEDL 240
rat         KNPCNGAVNTPDAFLGLSNLTHLSLKYNLTVPRQLPSPSLEYLLLSYNLIIVKLGAEDL 240
*** * : : * . : * * . * * * * * * * * * * * * * * * * * * * * * * * * * * * *

feline      ANLTALRVLDVGGNCRCDHARNPCMECPKGFPHLPDFTFSLHNLHLEGLVLKDSSLYNLN 300
canine      ANLTALRVLDVGGNCRCDHARNPCRECPKGFPLHPNTFGHLSHLEGLVLKDSSLYSLD 300
bovine      ANLTALRVLDVGGNCRCDHARNPCRECPKNFPLHPDFTFSLSRLEGLVLKDSSLYKLE 299
mouse       ANLTALRVLDVGGNCRCDHARNPCRECPKNFPLHPDFTFSLSRLEGLVLKDSSLYKLE 299
ovine       ANLTALRVLDVGGNCRCDHARNPCRECPKNFPLHPDFTFSLSRLEGLVLKDSSLYKLE 299
porcine     ANLTALRVLDVGGNCRCDHARNPCRECPKDHPLHSDFTFSLSRLEGLVLKDSSLYNLD 299
horse       ANLTALRVLDVGGNCRCDHARNPCVECPHFKFPLHSDFTFSLSRLEGLVLKDSSLYQLN 300
human       ANLTALRVLDVGGNCRCDHARNPCMECPRHFPQLHPDFTFSLSRLEGLVLKDSSLYSWLN 300
rat         ANLTSLRMLDVGGNCRCDHAPDLCTECRQKSLDLHPQTFHLSHLEGLVLKDSSLSHSLN 300
*** : * : * * * * * * * * * * : * * : . * : * * * : * * * * * * * *

feline      PRWFHALGNLMVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNYHKKVSFAHLHLAPSF 360
canine      PRWFHGLGNLMVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNYHKKVSFAHLHLASSF 360
bovine      KDWFRGLGRQLQVLDLSENFLYDYITKTTFNDLTQLRLNLSFNYHKKVSFAHLHLASSF 359
mouse       KDWFRGLGRQLQVLDLSENFLYDYITKTTFNDLTQLRLNLSFNYHKKVSFAHLHLASSF 359
ovine       KDWFRGLGRQLQVLDLSENFLYDYITKTTFIRNLTQLRLNLSFNYHKKVSFAHLQLAPSF 359
porcine     TRWFRGLDRLQVLDLSENFLYDCITKTTFQGLARLRLNLSFNYHKKVSFAHLHLAPSF 359
horse       PRWFRGLGNLTVLDLSENFLYDCITKTTFQGLAQRLRLNLSFNYHKKVSFAHLTLAPSF 360
human       ASWFRGLGNLTVLDLSENFLYKICITKTTFQGLTQLRLNLSFNYQKRVSAHLHLAPSF 360
rat         SKWFQGLANLTVLDLSENFLYIESINKTSAFQNLRLRLKLDLSFNYCKKVSFAHLHLASSF 360
* : * . * * * * * * * * * * . * * . * : * * * : * * * * * * * * * *

```

[illegible]

**Figure 1**  
**(3/3)**

feline	SFFALATRLRELNLSANALKTVEPSWFGSLAGTLKVLVDVTGNPLHCACGAAFVDFLLEVQ	778
canine	SFFALAVRLRELNLSANALKTVEPSWFGSLAGALKVLVDVTANPLHCACGATFVDFLLEVQ	780
bovine	GFFVRATRLIELNLSANALKTVDPWSWFGSLAGTLKILVDVSANPLHCACGAAFVDFLLERQ	776
mouse	GFFVRATRLIELNLSANALKTVDPWSWFGSLAGTLKILVDVSANPLHCACGAAFVDFLLERQ	776
ovine	GFFVLANRLKELNLSANALKTVDPWFGRITETLNILVDVSANPLHCACGAAFVDFLLEMQ	776
porcine	GFFALAKQLEELNLSANALKTVEPSWFGSMVGNLKVLDVSANPLHCACGATFVGFLLEVQ	777
horse	GFFALATRLRELNLSANALRTEEPSWFGFLAGSLEVLVDVSANPLHCACGAAFVDFLLQVQ	778
human	GFFSKAKELRELNLSANALKTVDPWSWFGPLASALQILVDVSANPLHCACGAAFMDFLLEVQ	778
rat	AFFALAVELKEVNLSHNILKTVDRSWFGPIVMNLTVLDVSSNPLHCACGAPFVDLLLEVQ	779
	. ** * . * * : * * * * : * * * : . * : * * * : . * * * * * * * * * * : . * * * : *	
feline	AAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFG	838
canine	AAVPGLPSPVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCF	840
bovine	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFG	836
mouse	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETSLDCFG	836
ovine	AAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFG	836
porcine	AAVPGLPSPVKCGSPGQLQGRSIFAQDLRLCLDETSLWNCFG	837
horse	AAVPGLPSPVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG	838
human	AAVPGLPSPVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFG	838
rat	TKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG	839
	****. * . **** * * * * * : * * * * * * * * * * . * * * : * * * : . * * * : *	
feline	CGWDLWYCFHLCLAWLPRRGRR--RGADALPYDAFVVDKAQSAVADWVYNELRVLEER	896
canine	CGWDLWYCFHLCLAWLPRRGRR--RGVDALAYDAFVVDKAQSSVADWVYNELRVQLEER	898
bovine	CGWDLWYCFHLCLAWLPRRRRQ--RGEDTLLYDAVVVDKQSAVADWVYNELRVQLEER	894
mouse	CGWDLWYCFHLCLAWLPRRRRQ--RGEDTLLYDAVVVDKQSAVADWVYNELRVQLEER	894
ovine	CGWDLWYCFHLCLAWLPRRRRQ--RGEDTLLYDAFVVDKAQSAVADWVYNELRVQLEER	894
porcine	CGWDLWYCFHLCLAWLPHRGQR--RGADALFYDAFVVDKAQSAVADWVYNELRVQLEER	895
horse	CGWDLWYCFHLCLAWLPRRGWQ--RGADALSYDAFVVDKAQSAVADWVYNELRVLEER	896
human	CGWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVDKQSAVADWVYNELRGQLEEC	898
rat	CGWDVWYCFHLCLAWLPLTRGR--RSAQALPYDAFVVDKAQSAVADWVYNELRVLEER	898
	****. * * * * * * * * * * . * . : * * * * * * * * * * . * * * * * * * * * * : * * *	
feline	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQORL	956
canine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQORL	958
bovine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLHDHTDRVSGLLRASFLLAQORL	954
mouse	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLHDHTDRVSGLLRASFLLAQORL	954
ovine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTMFVLHDHTDRVSGLLRASFLLAQORL	954
porcine	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQORL	955
horse	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQORL	956
human	RGRRALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQORL	958
rat	RGRRALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDKVSGLLRTSFLLAQORL	958
	*** * * * * * * * * * * : * * * * * * * * * * : * * * * * * * * * * : * * * * * * * * * * :	
feline	LEDKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQSFQAQLGTALTRDNQ	1016
canine	LEDKDVVVLVILCPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQSFQAQLGTALTRDNR	1018
bovine	LEDKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQSFWANLGIALTRDNR	1014
mouse	LEDKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQSFWANLGIALTRDNR	1014
ovine	LEDKDVVVLVILRPAAYRSRYVRLRQRLCRQSVLLWPHQPSGQSFWANLGIALTRDNR	1014
porcine	LEDKDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQPSGQSFQAQLGTALTRDNH	1015
horse	LEDKDVVVLVILSPDARRSRYVRLRQRLCRQSVLFWPHQPSGQSFQAQLGMALTRDNR	1016
human	LEDKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQSFQAQLGMALTRDNH	1018
rat	LEDKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLFWPHQPSGQSFQAQLSTALTRDNH	1018
	***** * . * * * * * * * * * * : * * * * * * * * * * : * * * * * * * * * * :	
feline	HFYNQNFRCGPTTAE-----	1031
canine	HFYNQNFRCGPTTA-----	1032
bovine	HFYNRNFCRGPTTAE-----	1029
mouse	HFYNRNFCRGPTTAE-----	1032
ovine	HFYNRNFCRGPTTAE-----	1029
porcine	HFYNRNFCRGPTTAE-----	1030
horse	HFYNQNFRCGPTMAE-----	1031
human	HFYNRNFCQGPTAE-----	1032
rat	HFYNRNFCRGPTAE-----	1032
	****. * * * * *	

Figure 2

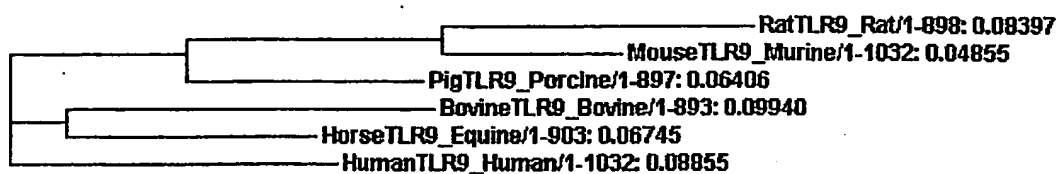
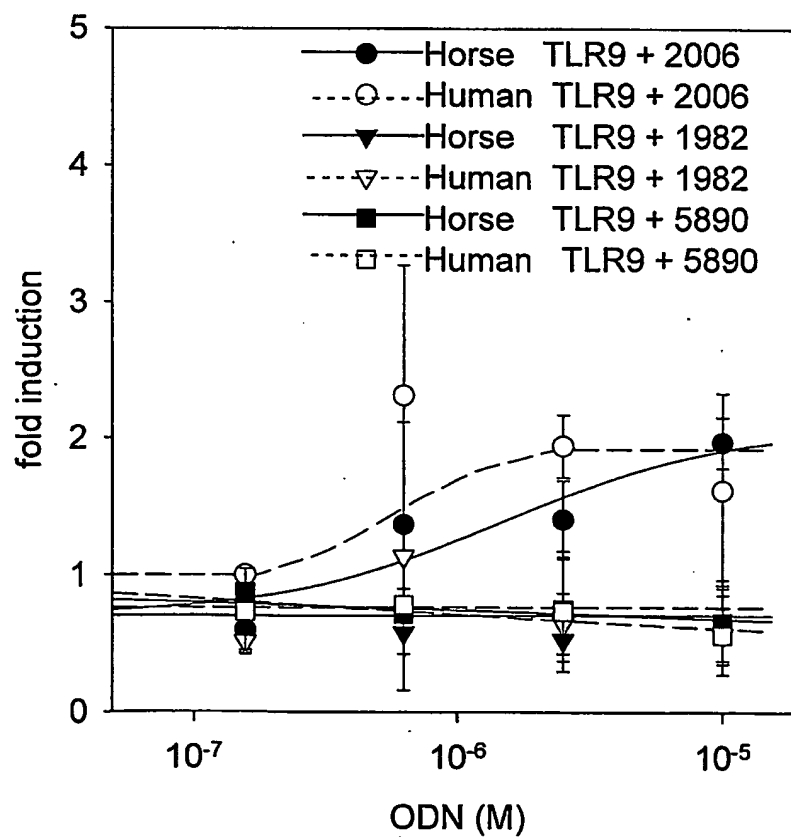


Figure 3



## SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH  
University of Saskatchewan  
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040WO00

<150> US 60/412,479

<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1

<211> 1032

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
130 135 140



Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610	615	620
Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys		
625	630	635 640
Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu		...
	645	650 655
Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser		
	660	665 670
Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn		
	675	680 685
Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu		
	690	695 700
Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala		
	705	710 715 720
Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn		
	725	730 735
Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn		
	740	745 750
Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly		
	755	760 765
Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly		
	770	775 780
Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg		
	785	790 795 800
Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser		
	805	810 815
Arg Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Thr Val		
	820	825 830
Leu Pro Leu Leu Gln His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe		
	835	840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser  
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser  
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 2  
 <211> 821  
 <212> PRT  
 <213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn  
 50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met  
 100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro  
 180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser  
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe  
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala  
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu  
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu  
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala  
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr  
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val  
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser  
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala  
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp  
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu  
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser  
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val  
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly  
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe  
610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys  
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu  
645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser  
660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn  
675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

[illegible]



gcccccgacc tctgtacaga atgccggcag aagtccttg atctgcaccc tcagactttc 840  
 catcacctga gccacettga aggcctggtg ctgaaggaca gttctctcca ctcgctgaac 900  
 tccaagtggg tccaggggtct ggcgaaacctc tcggtgctgg acctaaagcga gaactttctc 960  
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020  
 ctgtccttca attactgcaa gaaggatatcg ttcgcccgc tccacctggc aagttccttc 1080  
 aagagcctgg tgcgctgca ggagctgaac atgaacggca tcttcttcg cttactcaac 1140  
 aagaacacgc tcaggtgggt ggctggtctg cccaagctcc acacgctgca ccttcaaattg 1200  
 aatttcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260  
 gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320  
 gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccgagc tctcccgagc 1380  
 actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440  
 tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccattctccag 1500  
 tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccc 1560  
 ctgaccaacc tgaagggtgt ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620  
 tcgttcagtg agtcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680  
 agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740  
 cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800  
 gtggagtatc tggacttcag cggcaacggt gtgggcccga tgtgggacga ggaggacctt 1860  
 tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920  
 ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980  
 ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040  
 cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt 2100  
 ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160  
 ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220  
 gtggatcgct cctggtttgg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280  
 aacctctgc attgtgcctg cgggtgcaccc tttgtagact tactgctgga agtgcagacc 2340  
 aagggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400  
 agcatctttg cgcaagacct gcggtgtgtc ctggatgacg tcctttctcg ggactgcttt 2460  
 ggcctttcac tcctggctgt ggccgtgggc acggtgttgc ctttactgca gcatctctgc 2520  
 ggctgggacg tctggtactg tttccatctg tgccctggcat ggctacctt gctgaccgct 2580

ggccggcgca gcgccaagc tctcccttat gatgccttcg tgggtgttcga taaggcgag 2640  
 agcgcggttg ctgactgggt gtataacgag cttcgagtgc ggctagagga gcggcgcggt 2700  
 cgccgagccc tacgcttggt tctggaggac cgagattggc tgcctggcca gacactcttc 2760  
 gagaacctct gggcctccat ctatggcagc cgcaagactc tgtttggtgct ggcccacacg 2820  
 gacaaggtca gtggcctcct gcgcaccagc ttctgtgttg ctcagcagcg cctgctggag 2880  
 gaccgcaagg acgtggtggt gttggtgatc ctgcgccttg atgcccaccg ctcccgctac 2940  
 gtgcgactgc gccagcgctt ctgccgccag agtgtgtctt tctggcccca tcagcccaac 3000  
 gggcagggca gcttctgggc ccagctgagt acagccctga ctagggacaa ccaccacttc 3060  
 tataaccgga acttctgccc gggacctaca gcagaatag 3099

<210> 4  
 <211> 2463  
 <212> DNA  
 <213> Rattus norvegicus

<400> 4  
 atggttctct gtgcaggac cctgcacccc ttgtctctcc tggtagaggc cgcagtgttg 60  
 gctgaggctc tggccctggg taccctgcct gccttctac cctgtgaact gaagcctcat 120  
 ggctggtag actgcaactg gctcttcttg aagtctgtgc ctcaattctc tgccgcagaa 180  
 ccccggtcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240  
 ctogactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300  
 cctggcctca gcccttgca cttctcctgc cgcagacca ttgagcccaa aaccttcttg 360  
 gctatgcgca tgcctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420  
 ctgccagct ccctgacgaa tctgagccta agccacacca acatcctggg actcgatgcc 480  
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540  
 aagaaccctt gcaacggggc ggtgaacgtg acccggagc ccttctctgg cttagcaaac 600  
 ctcaacctact tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctgct gtcctataac ctcatcgta agctgggggc cgaagacctt 720  
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780  
 gccccgacc tctgtacaga atgccggcag aagtcccttg atctgcaccc tcagactttc 840  
 catcaacctg gccaccttga aggcctggtg ctgaaggaca gttctctcca ctgctgaac 900  
 tccaagtggg tccaggggtc ggcgaaacct tcggtgtgtg acctaagcga gaactttctc 960  
 tacgagagca tcaacaaaac cagcgccctt cagaacctga cccgtctgcg caagctcgac 1020

```

ctgtccttca attactgcaa gaaggtatcg ttcgcccgcc tccacctggc aagttccttc 1080
aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140
aagaacacgc tcaggtggct ggctggtctg cccaagctcc acacgctgca ccttcaaattg 1200
aatattcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccagc 1380
actcccgctc caaagaactt catggtcagg tgtaagaacc tcagattcac catggacctg 1440
tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag 1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccg 1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740
cttagcctgg cacacaatga cattcacagc cgcggtgcct cagcctcta cagcacctca 1800
gtggagtatc tggacttcag cggcaacggt gtgggccgca tgtgggacga ggaggacctt 1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt 2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220
gtggatcgct cctggtttgg gccatttgat atgaacctga cggttctaga cgtgagcagc 2280
aaccctctgc attgtgcctg cgggtgcaccc tttgtagact tactgctgga agtgcagacc 2340
aagggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400
agcatctttg cgcaagacct ggggctgtgc ctggatgacg tcctttctcg ggactgcttt 2460
ggc 2463

```

```

<210> 5
<211> 1030
<212> PRT
<213> Sus scrofa

<400> 5

```

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15  
 Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30  
 Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45  
 Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60  
 Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80  
 Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110  
 Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125  
 Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140  
 Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160  
 His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175  
 Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190  
 Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205  
 Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220  
 Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705		710		715		720
Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu						
	725			730		735
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys						
	740			745		750
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr						
	755			760		765
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro						
	770			775		780
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile						
	785			790		795
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn						
	805			810		815
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro						
	820			825		830
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu						
	835			840		845
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala						
	850			855		860
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val						
	865			870		875
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg						
	885			890		895
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro						
	900			905		910
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg						
	915			920		925
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu						
	930			935		940

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys  
 945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg  
 965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp  
 980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr  
 995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys  
 1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 6  
 <211> 819  
 <212> PRT  
 <213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val  
 1 5 10 15

Thr Ala Leu Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr  
 100 105 110



Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr  
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro  
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg  
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg  
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln  
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu  
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro  
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp  
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg  
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg  
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn  
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser  
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro  
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met  
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu  
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln  
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp  
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln  
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His  
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His  
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu  
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu  
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg  
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe  
 705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu  
 725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys  
 740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr  
 755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro  
 770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile  
 785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn  
 805 810 815

Cys Phe Gly

<210> 7  
 <211> 3352  
 <212> DNA  
 <213> Sus scrofa

<400> 7  
 gagcacgaac atccttccact gtagctgctg cccggctctgc cagccagacc ctttgagaa 60  
 gacccactc cctgtcatgg gccccgctg caccctgcac cccctttctc tcctggtgca 120  
 ggtgacagcg ctggctgagg ctctggccca gggcaggctg cctgccttcc tgccctgtga 180  
 gctccagccc cacggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt 240  
 ctggcgaggc gcgccccggg ccaacgtcac cagcctctcc ttactctcca accgcatcca 300  
 ccactgcac gactccgact tcgtccacct gtccagccta cgaactctca acctcaagtg 360  
 gaactgcccc cgggctggcc tcagcccat gcacttcccc tgccacatga ccatcgagcc 420  
 caacaccttc ctggccgtgc ccacctgga ggagctgaac ctgagctaca acagcatcac 480  
 gaccgtgcct gccctgcccg actccctcgt gtccctgtcg ctgagccgca ccaacatcct 540  
 ggtgctagac cccaccacc tcactggcct acatgccctg cgctacctgt acatggatgg 600  
 caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgccctcct 660  
 cggcctgggc aacctcacac atctctcact caagtacaac aatctcacgg aggtgccccg 720  
 cagcctgccc cccagcctgg agacctgct gttgtcctac aaccacattg tcacctgac 780  
 gcctgaggac ctggccaatc tgactgccct gcgcgtgctt gatgtggggg ggaactgccg 840  
 ccgctgtgac catgccccga accctgcag ggagtgccca aaggaccacc ccaagctgca 900  
 ctctgacacc ttccagccacc tgagccgcct cgaaggcctg gtgttgaaag acagttctct 960  
 ctacaacctg gacaccaggt ggttccgagg cctggacagg ctccaagtgc tggacctgag 1020  
 tgagaacttc ctctacgact gcatcaccaa gaccacggcc ttccagggcc tggcccgact 1080  
 gcgcagcctc aacctgtcct tcaattacca caagaaggct tcctttgcc acctgcacct 1140  
 ggcaccctcc tttgggcacc tccggtccct gaaggagctg gacatgcatg gcatcttctt 1200  
 ccgctcgctc agtgagacca cgctccaacc tctgggtcaa ctgcctatgc tccagacct 1260  
 gcgcctgcag atgaacttca ttaaccaggc ccagctcagc atctttgggg ccttccctgg 1320  
 cctgctgtac gtggacctat cggacaaccg catcagcgga gctgcaaggc cagtggccat 1380  
 tactagggag gtggatggta gggagagggt ctggctgcct tccaggaacc tcgctccacg 1440  
 tccactggac actctccgct cagaggactt catgccaaac tgcaaggcct tcagcttcac 1500

cttggacctg tctcggaaca acctggtgac aatccagtcg gagatgtttg ctgcctctc 1560  
 acgcctcgag tgcctgcgcc tgagccacaa cagcatctcc caggcgggtca atggctctca 1620  
 gtttgtgccg ctgaccagcc tgcgggtgct ggacctgtcc cacaacaagc tggacctgta 1680  
 tcacggggcg tcgttcacgg agctgccgcg cctggaagca ctggacctca gctacaatag 1740  
 ccagcccttt accatgcagg gtgtgggcca caacctcagc ttctgggcc agctgccgcg 1800  
 cctgcgtac ctgacctgg cgcaaatga catccatagc cgagtgtccc agcagctctg 1860  
 tagcgctca ctgtgcgcc tggactttag cggcaacgat ctgagccgga tgtgggctga 1920  
 gggagacctc tatctccgct tcttccaagg cctaagaagc ctagtctggc tggacctgtc 1980  
 ccagaaccac ctgcacacc tcctgccagc tgccctggac aacctccca aaagcctgaa 2040  
 gcatctgcat ctccgtgaca ataacctggc cttcttcaac tggagcagcc tgacctctc 2100  
 gccaagctg gaaacctgg acttggtgg aaaccagctg aaggccctaa gcaatggcag 2160  
 cctgccatct ggcaccagc tgcggaggct ggacctcagt ggcaacagca tcggctttgt 2220  
 gaacctggc ttctttgcc tggccaagca gttagaagag ctcaacctca gcgccaatgc 2280  
 cctcaagaca gtggagccct cctggtttg ctgatgggtg ggcaacctga aagtccatga 2340  
 cgtgagcgcc aacctctgc actgtgcctg tggggcgacc ttctgggct tcctgctgga 2400  
 ggtacaggct gccgtgcctg ggctgccag ccgcgtcaag tgtggcagtc cggggcagct 2460  
 ccagggccat agcatctttg cgcaagacct gcgctctgc ctggatgaga ccctctctg 2520  
 gaactgtttt ggcattctgc tgctggccat ggccctgggc ctggttgctgc ccatgctgca 2580  
 ccacctctgc ggctgggacc tctggtactg cttccacctg tgctggcct ggctgcccc 2640  
 ccgagggcag cggcggggcg cagacgccct gttctatgat gccttctggt tctttgacaa 2700  
 agctcagagt gctgtggccg actgggtgta caacgagctg cgggtgcagc tggaggagcg 2760  
 ccgtgggcgc cgcgactgc gcctgtgcct ggaggagcga gactggttac ctggcaagac 2820  
 gctcttcgag aacctgtggg cctcagtcta cagcagccgc aagacctgt ttgtgctggc 2880  
 ccacacggac cgtgtcagcg gcctcttgcg tgccagttc ctgctggccc agcagcgct 2940  
 gctggaggac cgcaaggacg ttgtagtgct ggtgatcctg cgcgccgatg cctaccgctc 3000  
 ccgtacgtg cggtgcgcc agcgctctg ccgccagagt gtcctctct ggccccacca 3060  
 gccccgtggg cagggcagct tctgggcca gctgggcaca gccctgacca gggacaacca 3120  
 ccacttctat aaccggaact tctgccggg cccacgaca gccgaatagc actgagtgc 3180  
 agcccagttg cccagcccc cctggatttg cctctctgcc tgggggtgcc caacctgctt 3240  
 tgctcagcca caccactgct ctgctccctg tccccacc cccccccag cctggcatgt 3300

aacatgtgcc caataaatgc taccggaggg ccaagaaaaa aaaaaaaaaa aa 3352

<210> 8

<211> 2457

<212> DNA

<213> Sus scrofa

<400> 8

atggggcccc gctgcaccct gcaccccctt tctctcctgg tgcaggtgac agcgctggct 60  
 gcggctctgg cccagggcag gctgcctgcc ttcttgccct gtgagctcca gccccacggc 120  
 ctggtgaact gcaactggct cttcctgaag tccgtgcccc acttctcggc ggcagcgccc 180  
 cgggccaacg tcaccagcct ctcttactc tccaaccgca tccaccacct gcaegactcc 240  
 gacttcgtcc acctgtccag cctacgaact ctcaacctca agtggaactg cccgccggct 300  
 ggctcagcc ccattgcaact cccctgccac atgaccatcg agcccaaacac cttcctggcc 360  
 gtgcccaccc tggaggagct gaacctgagc tacaacagca tcacgaccgt gcctgccttg 420  
 cccgactccc tcgtgtccct gtcgtgagc cgcaccaaca tcctggtgct agaccccacc 480  
 cacctcactg gcctacatgc cctgcgtac ctgtacatgg atggcaactg ctactacaag 540  
 aacccctgcc agggggcgct ggagggtgtg ccgggtgccc tcctcggcct gggcaacctc 600  
 acacatctct cactcaagta caacaatctc acggagggtgc cccgcagcct gccccccagc 660  
 ctggagaccc tgctgttgct ctacaaccac attgtcacc tgacgcctga ggacctggcc 720  
 aatctgactg ccctgcgctg gcttgatgtg ggggggaact gccgccgctg tgacctgcc 780  
 cgcaaccctc gcaggagtg cccaaaggac caccccaagc tgcactctga caccttcagc 840  
 cacctgagcc gcctcgaagg cctggtgttg aaagacagtt ctctctacaa cctggacacc 900  
 aggtggttcc gaggcctgga caggctccaa gtgctggacc tgagtgagaa cttcctctac 960  
 gactgcatca ccaagaccac ggcttccag ggctggccc gactgcgcag cctcaacctg 1020  
 tccttcaatt accacaagaa ggtgtccttt gccacctgc acctggcacc ctcctttggg 1080  
 cacctccggt ccctgaagga gctggacatg catggcatct tcttcgctc gctcagttag 1140  
 accacgctcc aacctctggt ccaactgct atgtccaga ccctgcgcct gcagatgaac 1200  
 ttcattaacc agggccagct cagcatcttt ggggccttcc ctggcctgct gtacgtggac 1260  
 ctatcggaca accgcatcag cggagctgca aggccagtg ccattactag ggagggtgat 1320  
 ggtagggaga gggctctggct gccttccagg aacctcgctc cactccact ggacactctc 1380  
 cgctcagagg acttcatgcc aaactgcaag gccttcagct tcaccttga cctgtctcgg 1440  
 aacaacctgg tgacaatcca gtcggagatg tttgctcgcc tctcacgcct cgagtgcctg 1500

cgctgagcc acaacagcat ctcccaggcg gtcaatggct ctcagtttgt gccgctgacc 1560  
 agcctgcggg tgctggacct gtcccacaac aagctggacc tgtatcacgg gcgctcgttc 1620  
 acggagctgc cgcgcctgga agcactggac ctcagctaca atagccagcc ctttaccatg 1680  
 caggggtgtgg gccacaacct cagcttcgtg gccagctgc ccgccctgcg ctacctcagc 1740  
 ctggcgcaaca atgacatcca tagccgagtg tcccagcagc tctgtagcgc ctcactgtgc 1800  
 gccctggact ttagcggcaa cgatctgagc cggatgtggg ctgagggaga cctctatctc 1860  
 cgcttcttcc aaggcctaag aagcctagtc tggctggacc tgtcccagaa ccacctgcac 1920  
 accctcctgc cacgtgccct ggacaacctc cccaaaagcc tgaagcatct gcatctccgt 1980  
 gacaataacc tggccttctt caactggagc agcctgacct tctgcccac gctggaaacc 2040  
 ctggacttgg ctggaaacca gctgaaggcc ctaagcaatg gcagcctgcc atctggcacc 2100  
 cagctgcgga ggctggacct cagtggcaac agcatcggct ttgtgaacct tggcttcttt 2160  
 gccctggcca agcagttaga agagctcaac ctcagcgcca atgccctcaa gacagtggag 2220  
 ccctcctggt ttggctcgat ggtgggcaac ctgaaagtcc tagacgtgag cgccaacct 2280  
 ctgcactgtg cctgtggggc gaccttcgtg ggcttcctgc tggaggtaca ggctgccgtg 2340  
 cctgggctgc ccagccgcgt caagtgtggc agtccggggc agctccaggg ccatagcatc 2400  
 ttgcgcaag acctgcgcct ctgcctggat gagaccctct cgtggaactg ttttggc 2457

<210> 9  
 <211> 1029  
 <212> PRT  
 <213> Bos taurus

<400> 9

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr



305	310	315	320
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg	325	330	335
Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His	340	345	350
Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu	355	360	365
Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln	370	375	380
Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn	385	390	395
Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu	405	410	415
Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro	420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu	435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp	450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn	465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu	485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly	500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His	515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln	530	535	540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
 850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala  
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg  
 930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
 965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
 980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala  
 995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
 1010 1015 1020

Gly Pro Thr Thr Ala Glu  
1025

<210> 10  
<211> 818  
<212> PRT  
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu  
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe  
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr  
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly  
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg  
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln  
 370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu		
435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp		
450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn		
465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu		
485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly		
500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His		
515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln		
530	535	540
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln		
545	550	555
Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg		
565	570	575
Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys		
580	585	590
Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu		
595	600	605
Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly		
610	615	620
Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr		
625	630	635
Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu		
645	650	655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val  
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

<210> 11

<211> 3191

<212> DNA

<213> Bos taurus

<400> 11

gggaagtggg cgccaagcat ccttcctgac agctgcctcc caacctgccc gccagaccct	60
ctggagaagc cgcattccct gtcattgggc cctactgtgc cccgcacccc ctttctctcc	120
tgggtgcaggc ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttcctgc	180
cctgtgagct ccagcccat ggtcagggtg actgcaactg gctgttcctg aagtctgtgc	240
cgcacttttc ggctggagcc ccccgggcca atgtcaccag cctctcctta atctccaacc	300

gcatccacca cttgcatgac tctgacttcg tccacctgtc caacctgcgg gtcctcaacc 360  
 tcaagtggaa ctgcccgcg gccggcctca gcccctatgca cttcccctgc cgtatgacca 420  
 tcgagcccaa caccttcctg gctgtgcca ccctggagga gctgaacctg agctacaacg 480  
 gcatcacgac cgtgcctgcc ctgcccagtt ccctcgtgtc cctgtcgctg agccacacca 540  
 gcatcctggg gctaggcccc acccaacttca cgggcctgca cgccctgcgc tttctgtaca 600  
 tggacggcaa ctgctactac atgaaccctt gccgcggggc cctggagggtg gccccaggcg 660  
 ccctcctcgg cctgggcaac ctcacgcacc tgtcgtcaa gtacaacaac ctcacggagg 720  
 tgccccgcg cctgcccccc agcctggaca ccctgctgct gtccataaac cacattgtca 780  
 ccctggcacc cgaggacctg gccaacctga ctgcccctgc cgtgcttgac gtgggtggga 840  
 actgccgcg ctgcgaccat gcccgcaacc cctgcaggga gtgcccagg aacttccccca 900  
 agctgcaccc tgacaccttc agtcacctga gcgcctcga aggcctgggtg ttgaaggaca 960  
 gttctctcta caaactagag aaagattggg tccgcggcct gggcaggctc caagtgtcgt 1020  
 acctgagtga gaacttcctc tatgactaca tcaccaagac caccatcttc aacgacctga 1080  
 cccagctgcg cagactcaac ctgtccttca attaccacaa gaagggtgtc ttcgcccacc 1140  
 tgcacctagc gtccctcttt gggagtctgg tgtccctgga gaagctggac atgcacggca 1200  
 tcttcttcg ctccctcacc aacatcacgc tccagtcgtc gaccgggtg cccaagctcc 1260  
 agagtctgca tctgcagctg aacttcctca accaggccca gctcagcatc tttggggcct 1320  
 tcccagacct gctcttcgtg gacctgtcgg acaaccgcat cagcggagcc gcgacgccag 1380  
 cggccgcctt gggggagggtg gacagcaggg tggaagtctg gcgattgccc aggggcctcg 1440  
 ctccaggccc gctggacgcc gtcagctcaa aggacttcat gccaaagtgc aacctcaact 1500  
 tcaccttgga cctgtcacgg aacaacctgg tgacaatcca gcaagagatg tttaccgcc 1560  
 tctccgcct ccagtgcctg cgcctgagcc acaacagcat ctgcaggcg gttaatggct 1620  
 cccagttcgt gccgctgacc agcctgcgag tgctcgacct gtcccacaac aagctggacc 1680  
 tgtaccatgg gcgctcattc acggagctgc cgcagctgga ggcaactggac ctcagctaca 1740  
 acagccagcc cttcagcatg cagggcgtgg gccacaacct cagcttcgtg gccagctgc 1800  
 cctccctgcg ctacctcagc cttgcgcaca atggcatcca cagccgcgtg tcacagaagc 1860  
 tcagcagcgc ctggttgccg gccctggact tcagcggcaa ctccctgagc cagatgtggg 1920  
 ccgagggaga cctctatctc tgctttttca aaggcttgag gaacctggtc cagctggacc 1980  
 tgtccgagaa ccatctgcac accctcctgc ctgctcacct ggacaacctg cccaagagcc 2040



tgcggcagct gcgctctccg gacaataacc tggccttctt caactggagc agcctgaccg 2100  
 tcctgccccg gctggaagcc ctggatctgg caggaaacca gctgaaggcc ctgagcaacg 2160  
 gcagcctgcc gcctggcatc cggctccaga agctggacgt gagcagcaac agcatcggct 2220  
 tcgtgatecc cggcttcttc gtccgcgcga ctccgctgat agagcttaac ctcagcgcca 2280  
 atgccctgaa gacagtggat ccctcctggg tgggttcctt agcagggacc ctgaaaatcc 2340  
 tagacgtgag cgccaacccg ctccactgcg cctgcggggc ggcccttggt gacttcctgc 2400  
 tggagagaca ggaggccgtg cccgggctgt ccaggcgctg cacatgtggc agtccggggc 2460  
 agctccaggc cgcagcatc ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520  
 ccttggaactg ctttggcctc tcaactgctaa tgggtggcgt gggcctggca gtgcccattg 2580  
 tgcaccacct ctgtggctgg gacctctggg actgcttcca cctgtgtctg gccatttgc 2640  
 cccgacggcg gcggcagcgg ggcgaggaca ccctgctcta tgatgccgtc gtggtcttcg 2700  
 acaaggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760  
 agcgccgggg ggcgcggggc ctccgcctct gcctggagga gcgagactgg ctccctggta 2820  
 agacgctctt cgagaacctg tgggcctcgg tctacagcag ccgcaagacc atgttcgtgc 2880  
 tggaccacac ggaccgggtc agcggcctcc tgcgcgccag cttcctgctg gccagcagc 2940  
 gcctgttggg ggaccgcaag gacgtcgtag tgctgggtgat cctgcgcccc gccgcctatc 3000  
 ggtcccgcga cgtgcggctg cgccagcgcc tctgcgcga gagcgtcctc ctctggcccc 3060  
 accagcccag tggccagggt agtttctggg ccaacctggg catagccctg accagggaca 3120  
 accgtcactt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180  
 tgactgcccc g 3191

&lt;210&gt; 12

&lt;211&gt; 2454

&lt;212&gt; DNA

&lt;213&gt; Bos taurus

&lt;400&gt; 12

atgggcccct actgtgcccc gcacccccct tctctcctgg tgcaggcggc ggcactggca 60  
 gcggccctgg ccgagggcac cctgcctgcc ttctgcct gtgagctcca gcccattggt 120  
 caggtggact gcaactggct gttcctgaag tctgtgccgc acttttcggc tggagcccc 180  
 cgggccaatg tcaccagcct ctcttaata tccaaccgca tccaccactt gcatgactct 240  
 gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaaactg cccgcccggc 300  
 ggccctagcc ccatgcactt cccctgccgt atgaccatcg agcccaaac cttcctggct 360

gtgcccaccc	tggaggagct	gaacctgagc	tacaacggca	tcacgaccgt	gcctgcccctg	420
cccagttccc	tcggtgccct	gtcgctgagc	cacaccagca	tcctggtgct	aggccccacc	480
cacttcaccg	gcctgcacgc	cctgcgcttt	ctgtacatgg	acggcaactg	ctactacatg	540
aacccctgcc	cgcggggcct	ggaggtggcc	ccaggcgccc	tcctcggcct	gggcaacctc	600
acgcacctgt	cgtcaagta	caacaacctc	acggaggtgc	cccgccgcct	gccccccagc	660
ctggacaccc	tgctgctgtc	ctacaaccac	attgtcaccc	tggcaccgga	ggacctggcc	720
aacctgactg	ccctgcgcgt	gcttgacgtg	ggtagggaact	gccgcgcgtg	cgaccatgcc	780
cgcaaccctt	gcagggagtg	cccaaagaac	ttccccaagc	tgcaccctga	caccttcagt	840
cacctgagcc	gcctcgaagg	cctggtgttg	aaggacagtt	ctctctacaa	actagagaaa	900
gattggttcc	gcggcctggg	caggctccaa	gtgctcgacc	tgagtgagaa	cttcctctat	960
gactacatca	ccaagaccac	catcttcaac	gacctgaccc	agctgcgcag	actcaacctg	1020
tccttcaatt	accacaagaa	ggtgtccttc	gcccacctgc	acctagcgtc	ctcctttggg	1080
agtctggtgt	ccctggagaa	gctggacatg	cacggcatct	tcttcgcgtc	cctcaccaac	1140
atcacgctcc	agtcgctgac	cgggctgccc	aagctccaga	gtctgcatct	gcagctgaac	1200
ttcatcaacc	aggcccagct	cagcatcttt	ggggccttcc	cgagcctgct	cttcgtggac	1260
ctgtcggaca	accgcatcag	cggagccgcg	acgccagcgg	ccgccctggg	ggaggtggac	1320
agcaggggtg	aagtctggcg	attgcccagg	ggcctcgctc	caggcccgtc	ggacgcgcgc	1380
agctcaaagg	acttcatgcc	aagctgcaac	ctcaacttca	ccttggacct	gtcacggaac	1440
aacctggtga	caatccagca	agagatgttt	acccgcctct	cccgccctca	gtgcctgcgc	1500
ctgagccaca	acagcatctc	gcaggcggtt	aatggctccc	agttcgtgcc	gctgaccagc	1560
ctgcgagtgc	tgcacctgtc	ccacaacaag	ctggacctgt	accatgggcg	ctcattcacg	1620
gagctgccgc	agctggaggc	actggacctc	agctacaaca	gccagccctt	cagcatgcag	1680
ggcgtggggc	acaacctcag	cttcgtggcc	cagctgccct	ccctgcgcta	cctcagcctt	1740
gcgcacaatg	gcattccacag	cgcgtgtca	cagaagctca	gcagcgctc	gttgcgcgcc	1800
ctggacttca	gcggcaactc	cctgagccag	atgtgggccc	agggagacct	ctatctctgc	1860
tttttcaaag	gcttgaggaa	cctggtccag	ctggacctgt	ccgagaacca	tctgcacacc	1920
ctcctgcctc	gtcacctgga	caacctgccc	aagagcctgc	ggcagctgcg	tctccgggac	1980
aataacctgg	ccttcttcaa	ctggagcagc	ctgaccgtcc	tgcgccggct	ggaagccctg	2040
gatctggcag	gaaaccagct	gaaggccctg	agcaacggca	gcctgcccgc	tggcatccgg	2100
ctccagaagc	tggacgtgag	cagcaacagc	atcggtctcg	tgateccccg	cttcttcgtc	2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220  
 tcctgggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caaccgctc 2280  
 cactgcgcct gcggggcggc ctttgtggac ttcctgctgg agagacagga ggccgtgccc 2340  
 gggctgtcca ggcgcgtcac atgtggcagt cggggccagc tccagggccg cagcatcttc 2400  
 acacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13  
 <211> 1031  
 <212> PRT  
 <213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro  
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly  
 165 170 175  
 Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro  
 180 185 190  
 Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205  
 Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220  
 Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240  
 Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255  
 Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe  
 260 265 270  
 Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285  
 Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300  
 Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320  
 Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335  
 Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350  
 His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365  
 Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380  
 Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly  
 405 410 415  
 Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu  
 420 425 430  
 Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu  
 435 440 445  
 Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu  
 450 455 460  
 Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser  
 465 470 475 480  
 Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
 485 490 495  
 Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val  
 500 505 510  
 Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525  
 Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540  
 Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560  
 Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr  
 565 570 575  
 Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser  
 580 585 590  
 Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn  
 595 600 605  
 Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe  
 610 615 620  
 Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
                                 645                                650                                655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
                                 660                                665                                670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
                                 675                                680                                685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
                                 690                                695                                700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
                                 705                                710                                715                                720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
                                 725                                730                                735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
                                 740                                745                                750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
                                 755                                760                                765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
                                 770                                775                                780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
                                 785                                790                                795                                800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
                                 805                                810                                815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met  
                                 820                                825                                830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
                                 835                                840                                845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp  
                                 850                                855                                860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

- 40 -

35	40	45	
Phe	Leu	Lys	Ser
50			
Val	Pro	His	Phe
		55	
Ser	Ala	Ala	Ala
			60
Pro	Arg	Asp	Asn
Val	Thr	Ser	Leu
65			
Ser	Leu	Leu	Ser
	70		
Asn	Arg	Ile	His
		75	
His	His	Leu	His
			80
Asp			
Ser	Asp	Phe	Ala
Gln	Leu	Ser	Asn
85			
Leu	Gln	Lys	Leu
	90		
Asn	Leu	Lys	Trp
		95	
Asn	Cys	Pro	Pro
Ala	Gly	Leu	Ser
Pro	Met	His	Phe
	105		
Pro	Cys	His	Met
		110	
Thr	Ile	Glu	Pro
Asn	Thr	Phe	Leu
Ala	Val	Pro	Thr
Leu	Glu	Glu	Leu
	125		
Asn	Leu	Ser	Tyr
Asn	Gly	Ile	Thr
Thr	Val	Pro	Ala
Leu	Pro	Ser	Ser
130			
Leu	Val	Ser	Leu
Ile	Leu	Ser	Arg
Thr	Asn	Ile	Leu
Gln	Leu	Asp	Pro
145			
Thr	Ser	Leu	Thr
Gly	Leu	His	Ala
Leu	Arg	Phe	Leu
Tyr	Met	Asp	Gly
165			
Asn	Cys	Tyr	Tyr
Lys	Asn	Pro	Cys
Gly	Arg	Ala	Leu
Glu	Val	Ala	Pro
180			
Gly	Ala	Leu	Leu
Gly	Leu	Gly	Asn
Leu	Thr	His	Leu
Ser	Leu	Lys	Tyr
195			
Asn	Asn	Leu	Thr
Thr	Val	Pro	Arg
Ser	Leu	Pro	Pro
Ser	Leu	Glu	Tyr
210			
Leu	Leu	Leu	Ser
Tyr	Asn	His	Ile
Val	Thr	Leu	Ala
Pro	Glu	Asp	Leu
225			
Ala	Asn	Leu	Thr
Ala	Leu	Arg	Val
Leu	Asp	Val	Gly
Gly	Gly	Asn	Cys
Arg			
245			
Arg	Cys	Asp	His
Ala	Arg	Asn	Pro
Cys	Val	Glu	Cys
Pro	His	Lys	Phe
260			
Cys	Val	Glu	Cys
Pro	His	Lys	Phe
265			
Arg	Cys	Asp	His
Ala	Arg	Asn	Pro
Cys	Val	Glu	Cys
Pro	His	Lys	Phe
270			



Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu  
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly  
 405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu  
 420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu  
 435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu  
 450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe  
 610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu  
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser  
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp  
 805 810 815

Asp Cys Phe Gly  
 820

<210> 15  
 <211> 3391  
 <212> DNA  
 <213> Equus caballus

<400> 15  
 ctctgttctc tgagctgttg ccgctgaag ggactgagag cacaagcat cctcctctgc 60  
 agctgctgcc cagtgtgcca gctggaccct ctggatcatc tccactccc tgcatgggc 120  
 ccttgccatg gtgccctgca gccctgtct ctctgggtgc aggcggccat gctggcctg 180  
 gctctggccc aaggcaccct gcctcccttc ctgccctgtg agctccagcc ccacggcctg 240  
 gtgaactgca actggctgtt cctgaagtcc gtgcccact tctcagcagc agcaccctgg 300  
 gacaatgtca ccagccttcc cttgctctcc aaccgcatcc accacctcca cgactccgac 360  
 ttgcccacac tgtccaacct gcagaaactc aacctcaaat ggaactgccc gccagccggc 420  
 ctgagcccca tgcacttccc ctgccacatg accatcgagc ccaacacttt cctggctgta 480  
 cccaccctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgcctgccc 540  
 agtccctctg tgtccctgat cctgagccgc accaacatcc tgcagctaga cccaccagc 600  
 ctcacgggccc tgcattccct gcgcttccta tacatggatg gcaactgcta ctacaagaac 660  
 ccctgcgggc gggccctgga ggtggcccca ggcgcctcc ttggcctggg caacctcacc 720  
 cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc ccctagcctg 780  
 gagtacctgc tgttgccta caaccacatt gtcaccctgg cacctgagga cctggccaat 840  
 ctgactgccc tgcgtgtgct cgatgtgggt ggaaactgcc gccgctgtga ccatgcacgc 900  
 aaccctgcg tggagtgccc acataaatcc cccagctgc actccgacac cttcagccac 960

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga 1020  
 tggttccgtg gcctgggcaa cctcacagtg ctcgacctga gtgagaactt cctctacgac 1080  
 tgcatcacca aaaccaaggc attccagggc ctggcccagc tgcgaagact caacttgtcc 1140  
 ttcaattacc ataagaaggt gtccttcgcc cacctgacgc tggcaccctc cttcgggagc 1200  
 ctgctctccc tgcaggaact ggacatgcat ggcatcttct tccgctcact cagccagaag 1260  
 acgctccagc cactggcccg cctgcccattg ctccagcgtc tgtatctgca gatgaacttc 1320  
 atcaaccagg cccagctcgg catcttcaag gacttccttg gtctgcgcta catagacctg 1380  
 tcagacaacc gcatcagtgg agctgtggag ccggtggcca ccacagggga ggtggatggt 1440  
 gggaagaagg tctggctgac atccagggac ctactccag gccactgga cacccccagc 1500  
 tctgaggact tcatgccaaag ctgcaagaac ctgagcttca ccttggacct gtcacggaac 1560  
 aacctggtaa cagtccagcc agagatgttt gccagctct cgcgcctcca gtgcctgcmc 1620  
 ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc 1680  
 ctgcaggtgc tggacctgtc ccataacaaa ctggacctgt accatgggcm ctcgtttacg 1740  
 gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg 1800  
 ggtgtgggcm acaacctcag ctttgtggcm cagctgccca ccctgcgcta cctcagcctg 1860  
 gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtgggcm 1920  
 ctggacttca gcggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc 1980  
 ttcttccaag gcctgagaag cctaattccg ctagacctgt ccagaaatcg tctgcatacc 2040  
 ctcttgccat gcacctggg caacctcccc aagagcttgc agctgctgcm tctccgtaac 2100  
 aattacctgg ccttcttcaa ttggagcagc ctgacctcc tgcccaacct ggaaacctg 2160  
 gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcaccag 2220  
 ctccagaggc tggacgtcag caggaaacag atcatcttcg tggtccttg cttctttgct 2280  
 ctggccacga ggctgcgaga gctcaacctc agtgccaacg ccctcaggac agaggagccc 2340  
 tcctggtttg gtttcctagc aggtccctt gaagtccatg atgtgagcm caacctctg 2400  
 cactgcgcct gtggggcagc ctttgtggac ttctgctgc aggttcaggc tgccgtgcct 2460  
 ggtctgcccga gccgcgtcaa gtgtggcagt ccgggccagc tccagggcm cagcatcttc 2520  
 gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggctcttca 2580  
 ttgctggttg tggccctggg cctggccatg cctatgttgc accacctctg cggctgggac 2640  
 ctctgggtact gcttccacct gggcctggcm tggctgcccc ggcgggggtg gcagcgggcm 2700

gcggatgccc tgagctatga tgcctttgtg gtcttcgaca aggcacagag cgcagtggcc 2760  
gactgggtgt acaatgaact gcggtggtg ctagaggagc gccgtgggcg ccggggtgtc 2820  
cgcctgtgtc tggaggagcg tgactggcta cctggcaaga cgctgttcga aaacctgtgg 2880  
gcctcagtct acagcagccg caagatgctg tttgtgctgg cccacacgga ccaggtcagt 2940  
ggcctcttgc gtgccagctt cctgctggcc cagcagcgtc tgctggagga ccgcaaggac 3000  
gttgtggtgc tggtaatcct gagccctgac gcccgccgtt cccgttacgt ggggtgtgcg 3060  
cagcgcctct gccgccagag tgtcctcttc tggccccacc agcctagtgg ccagcgcagc 3120  
ttctggggcc agctaggcat ggccctgacc agggacaacc gccacttcta taaccagaac 3180  
ttctgccggg gcccgaagat ggctgagtag cacagagtga cagcctggca tgtacaaccc 3240  
ccagccctga ccttgctct ctgcctatga tgccagctc gccctactct gtgacgcccc 3300  
tgctctgct cgcgccacct caccctggc atacagcagg cactcaataa atgccactgg 3360  
caggccaaac agccaaaaa aaaaaaaaaa a 3391

<210> 16  
<211> 2460  
<212> DNA  
<213> Equus caballus

<400> 16  
atggggcctt gccatggtgc cctgcagccc ctgtctctcc tgggtgcaggc ggccatgctg 60  
gccgtgggtc tggcccaagg caccctgcct ccttctctgc cctgtgagct ccagccccac 120  
ggcctggtga actgcaactg gctgttcctg aagtccgtgc cccacttctc agcagcagca 180  
ccccgggaca atgtcaccag ccttctcttg ctctccaacc gcatccacca cctccacgac 240  
tccgactttg cccaactgtc caacctgcag aaactcaacc tcaaattggaa ctgcccgcga 300  
gccggcctca gcccctatgca cttcccctgc cacatgacca tcgagcccaa cacttctctg 360  
gctgtaccca ccctggagga gctgaacctg agctacaacg gcatcacgac tgtgctgcc 420  
ctgcccagct cctcgtgtc cctgatcctg agcgcacca acatcctgca gctagacccc 480  
accagcctca cgggcctgca tgccctgcgc ttcctataca tggatggcaa ctgctactac 540  
aagaaccctt gggggcgggc cctggaggtg gcccagcg ccctccttgg cctgggcaac 600  
ctcaccacac tgtcactcaa gtacaacaac ctcaaacgg tgccccgcag cctgccccct 660  
agcctggagt acctgctgtt gtctacaac cacattgtca ccctggcacc tgaggacctg 720  
gccaatctga ctgccctgcg tgtgctcgat gtgggtggaa actgccgcg ctgtgacct 780  
gcacgcaacc cctgcgtgga gtgccacat aaattcccc agctgcactc cgacaccttc 840

```

agccacctaa gccgcctaga aggcctcgtg ttgaaggata gttctctcta ccagctgaac      900
cccagatggg tccgtggcct gggcaacctc acagtgctcg acctgagtga gaacttcctc      960
tacgactgca tcacaaaaac caaggcattc cagggcctgg cccagctgcg aagactcaac     1020
ttgtccttca attaccataa gaagggtgtc ttgcgccacc tgacgctggc accctccttc     1080
gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttcgg ctcaactcagc     1140
cagaagacgc tccagccact ggccgcctg cccatgctcc agcgtctgta tctgcagatg     1200
aacttcatca accaggccca gctcggcatc ttcaaggact tccctgggtc gcgctacata     1260
gacctgtcag acaaccgcat cagtggagct gtggagccgg tggccaccac aggggaggtg     1320
gatggtgga agaaggtctg gctgacatcc agggacctca ctccaggccc actggacacc     1380
cccagctctg aggacttcat gccaaagtgc aagaacctca gcttcacctt ggacctgtca     1440
cggaacaacc tggtaacagt ccagccagag atgtttgccc agctctcgcg cctccagtgc     1500
ctgcgcctga gccacaacag catctcgagc gcggtcaatg gctcacagtt cgtgccactg     1560
accagcctgc aggtgctgga cctgtcccat aacaaactgg acctgtacca tgggcgctcg     1620
tttacggagc tgccgcgact ggaggccctg gacctcagct acaacagcca gcccttcagc     1680
atgcgggggtg tgggccacaa cctcagcttt gtggccagc tgcccaccct gcgctacctc     1740
agcctggcac acaatggcat ccacagccgt gtgtccagc agctctgcag cacctcgctg     1800
tgggccctgg acttcagcgg caattccctg agccagatgt gggctgaggg agacctctat     1860
ctccgcttct tccaaggcct gagaagccta atccggctag acctgtcca gaatcgctcg     1920
cataccctcc tgccatgcac cctgggcaac ctccccaaga gcttgcagct gctgcgtctc     1980
cgtaacaatt acctggcctt cttcaattgg agcagcctga ccctcctgcc caacctggaa     2040
acctggacc tggttggaac ccagctgaag gctctgagca atggcagcct gccttctggc     2100
accagctcc agaggctgga cgtcagcagg aacagcatca tcttcgtggg ccctggcttc     2160
tttgctctgg ccacgaggct gcgagagctc aacctcagt ccaacgccct caggacagag     2220
gagccctcct ggtttggttt cctagcaggc tcccttgaag tcctagatgt gagcgccaac     2280
cctctgcact gcgcctgtgg ggcagccttt gtggacttcc tgctgcaggt tcaggctgcc     2340
gtgcctggtc tgcccagccg cgtcaagtgt ggcagtccgg gccagctcca gggccgcagc     2400
atcttcgcac aagacctgcg cctctgcctg gacaagtccc tctcctggga ctgttttggg     2460

```

<210> 17

<211> 1029

<212> PRT

<213> Ovis aries

&lt;400&gt; 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr  
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn  
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu  
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr  
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn  
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly  
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn  
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu  
 210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala  
 225 230 235 240  
 Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg  
 245 250 255  
 Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro  
 260 265 270  
 Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu  
 275 280 285  
 Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg  
 290 295 300  
 Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr  
 305 310 315 320  
 Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg  
 325 330 335  
 Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350  
 Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365  
 Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380  
 Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400  
 Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415  
 Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430  
 Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445  
 Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460



Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met  
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys  
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu  
850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala  
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly  
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly  
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys  
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930                      935                      940  
 Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp  
 945                      950                      955                      960  
 Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr  
                     965                      970                      975  
 Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro  
                     980                      985                      990  
 His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala  
                     995                      1000                      1005  
 Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg  
                     1010                      1015                      1020  
 Gly Pro Thr Thr Ala Glu  
                     1025  
 <210> 18  
 <211> 818  
 <212> PRT  
 <213> Ovis aries  
 <400> 18  
 Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala  
 1                      5                      10                      15  
 Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu  
                     20                      25                      30  
 Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe  
                     35                      40                      45  
 Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val  
                     50                      55                      60  
 Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser  
 65                      70                      75                      80  
 Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn  
                     85                      90                      95  
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100	105	110
Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn		
115	120	125
Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu		
130	135	140
Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr		
145	150	155
His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn		
165	170	175
Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly		
180	185	190
Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn		
195	200	205
Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu		
210	215	220
Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala		
225	230	235
Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg		
245	250	255
Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro		
260	265	270
Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu		
275	280	285
Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg		
290	295	300
Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr		
305	310	315
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg		
325	330	335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His  
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu  
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg  
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn  
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu  
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro  
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp  
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp  
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn  
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu  
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly  
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr  
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln  
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln  
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg  
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys  
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu  
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly  
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr  
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu  
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr  
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu  
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val  
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile  
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg  
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys  
 805 810 815

Phe Gly

<210> 19  
 <211> 3199  
 <212> DNA  
 <213> Ovis aries

<400> 19  
 gtcggcacgg gaagtgagcg ccaagcatcc ttccctgcag ctgccgcca acttgcccgc 60  
 cagaccctct ggagaagccg cattccctgc catgggcccc tactgtgccc cgcaccccct 120  
 ttctctcctg gtgcaggcgg cggcgtggc agcagccctg gccagggca ccctgcctgc 180  
 cttcctgccc tgtgagctcc agccccggg taagggtgaac tgcaactggc tgttcctgaa 240  
 gtctgtgccc cgcttttcgg ccggagcccc cggggccaat gtcaccagcc tctccttaat 300  
 ctccaaccgc atccaccact tgcacgactc tgacttcgtc cacctgtcca acctgcgggt 360  
 cctcaacctc aagtggaact gcccgcggc cggcctcagc cccatgcaact tccccgccc 420  
 catgaccatc gagcccaaca ccttcttggc tgtgcccacc ctggaggagc tgaacctgag 480  
 ctacaatggc atcacgaccg tgccctgcct gccagttct ctcttatccc tgcctgtgag 540  
 ccgcaccagc atcctgggtc taggccccac ccacttcacc ggctgcacg ccctgcgctt 600  
 tctgtacatg gacggcaact gctactataa gaacccctgc cagcaggccg tggagggtggc 660  
 cccaggcgcc ctccctggcc tgggcaacct caccgacctg tcgctcaagt acaacaacct 720  
 caccggaggtg ccccgccgcc tgccccccag cctggacacc ctgctgctgt cctacaacca 780  
 catcatcacc ctggcaccgg aggacctggc caatctgact gccctgcgtg tgcttgatgt 840  
 gggcggggaac tgccgcgct gcgaccacgc ccgcaacccc tgcaggaggt gccaaagaa 900  
 cttccccaag ctgcaccctg acaccttcag ccacctgagc cgctcgaag gcctggtgtt 960  
 gaaggacagt tctctctaca aactagagaa agactgggtc cgcgccctgg gcaggctcca 1020  
 agtgctcgac ctgagtgaga acttcctcta tgactacatc accaagacca ccatcttcag 1080  
 gaacctgacc cagctgcgca gactcaacct gtccttcaat taccacaaga aggtgtcctt 1140  
 cgcccacctg caactggcac cctcctttgg gggcctgggt tccctggaga agctggacat 1200  
 gcacggcatc ttcttcgct ccctcaccia caccacgctc cgcccgctga ccagctgcc 1260  
 caagctccag agtctgagtc tgcagctgaa cttcatcaac caggccgagc tcagcatctt 1320  
 tggggccttc ccgagcctgc tcttcgtgga cctgtcggac aaccgcatca gcggagctgc 1380  
 gagggcgggtg gccgccctcg gggagggtgga cagcgggggt gaagtctggc ggtggccag 1440

```

gggcctcgct ccaggcccg cggccgcccgt cagcgcaaag gacttcatgc caagctgcaa 1500
cctcaacttc accttgacc tgtcacggaa caacctgggtg acgatccagc aggagatgtt 1560
taccgccttc tcccgctcc agtgctgcg cctgagccac aacagcatct cgcaggcggg 1620
taatggctcg cagttcgtgc cgctgacccg cctgcgagt ctcgacctgt cctacaacaa 1680
gctggacctg taccatgggc gctcgttcac ggagctgccg cagctggagg cactggacct 1740
cagctacaac agccagccct tcagcatgca gggcgtgggc cacaacctca gcttcgtggc 1800
ccagctgccg tccctgcgct acctcagcct tgcgcacaaac ggcatccaca gccgcgtgtc 1860
acagaagctc agcagcgcc cgtgcgcgc cctggacttc agcggcaact ccctgagcca 1920
gatgtgggccc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctgggtcca 1980
gctggacctg tccaagaacc acctgcacac cctcctgcct cgtcacctgg ataacctgcc 2040
caagagcctg cggcagctgc gtctccggga caataacctg gccttcttca actggagcag 2100
cctgactgtt ctgccccagc tggaagccct ggatctggcg ggaaaccagc tgaaggccct 2160
gagcaacggc agcctgccac ctggcaccgc gctccagaag ctggacgtga gcagcaacag 2220
catcggcttt gtgaccctg gcttctttgt ccttgccaac cggctgaaag agcttaacct 2280
cagcgccaac gccctgaaga cagtggatcc cttctgggtc ggctcgctta cagagacct 2340
gaatatacta gacgtgagcg ccaaccgcct cactgtgcc tcgggggcgg cctttgtgga 2400
cttctgctg gagatgcagg cgccgtgcc tgggctgtcc aggcgcgtca cgtgtggcag 2460
tccgggccag ctccagggcc gcagcatctt cgcacaggac ctgcgcctct gcctggatga 2520
gacctctcc ttggactgct ttggcttctc gctgctaata gtggcgttg gcctggcgg 2580
gccatgctg caccacctct gtggctggga cctgtggtac tgcttccacc tgtgtctggc 2640
ccatttgccc cgacggcggc ggcagcgggg cgaggacacc ctgctctacg atgccttcgt 2700
ggcttctgac aaggcgca ga gtgcagtggc cgactgggtg tacaacgagc tccgcgtgca 2760
gctggaggag cgccgcgggc gccggcgct ccgcctctgc ctggaggagc gagactggct 2820
ccctggcaag acgctcttcg agaacctgtg ggcctcggtc tacagcagcc gtaagacct 2880
gttcgtgctg gaccacacgg accgggtcag tggcctcctg cgcgccagct tctgctggc 2940
ccagcagcgc ctgttgagg accgcaagga tgcgtggtg ctggtgatcc tgcgccccgc 3000
cgctaccgg tccgctacg tgcggtgcg ccagcgctc tgccgcaga gcgtcctcct 3060
ctggccccac cagcccagtg gccaggtag cttctggggc aacctgggca tggccctgac 3120
cagggacaac cgccacttct ataaccggaa cttctgccgg ggcgccacga cagccgaata 3180

```



gcacagagtg actgcccag

3199

&lt;210&gt; 20

&lt;211&gt; 2454

&lt;212&gt; DNA

&lt;213&gt; Ovis aries

&lt;400&gt; 20

atgggcccct actgtgcccc gcaccccctt tctctcctgg tgcaggcggc ggcgctggca	60
gcagccctgg cccagggcac cctgcctgcc ttctgccct gtgagctcca gcccggggt	120
aaggtgaact gcaactggct gttcctgaag tctgtgccgc gcttttcggc cggagcccc	180
cgggccaatg tcaccagcct ctcttaatc tccaaccgca tccaccactt gcacgactct	240
gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaaactg cccgccggcc	300
ggcctcagcc ccatgcactt cccctgccgc atgaccatcg agcccaacac ctctctggct	360
gtgccacccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgccctg	420
cccagttctc tcgtatccct gtctgtgagc cgcaccagca tcctgggtgt aggccccacc	480
cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactataag	540
aaccctgcc agcaggccgt ggaggtggcc ccaggcgccc tccttggcct gggcaacctc	600
acgcacctgt cgtcaagta caacaacctc acggaggtgc cccgcgcct gccccccagc	660
ctggacaccc tgctgtgtc ctacaaccac atcatcacc tggcaccga ggacctggcc	720
aatctgactg ccctgcgtgt gcttgatgtg ggcgggaact gccgcgctg cgaccacgcc	780
cgaacccct gcagggagtg cccaaagaac ttccccaaagc tgcacctga caccttcagc	840
cacctgagcc gcctcgaagg cctgggtgtg aaggacagtt ctctctacaa actagagaaa	900
gactggttcc ggggcctggg caggctccaa gtgctcgacc tgagtgagaa ctctctctat	960
gactacatca ccaagaccac catcttcagg aacctgacct agctgcgcag actcaacctg	1020
tccttcaatt accacaagaa ggtgtccttc gccacctgc aactggcacc ctcttttggg	1080
ggcctggtgt ccctggagaa gctggacatg cacggcatct tcttcgctc cctcaccaac	1140
accacgctcc ggccgctgac ccagctgccc aagctccaga gtctgagtct gcagctgaac	1200
ttcatcaacc aggccgagct cagcatcttt ggggccttcc cgagcctgct ctctgtggac	1260
ctgtcggaca accgcatcag cggagctgcg aggccggtgg ccgccctcgg ggaggtggac	1320
agcggggtgg aagtctggcg gtggccagg gccctcgctc caggcccgct ggccgcgctc	1380
agcgcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac	1440
aacctggtga cgatccagca ggagatgttt acccgctct cccgcctcca gtgcctgcgc	1500

ctgagccaca acagcatctc gcaggcggtt aatggctcgc agttcgtgcc gctgacccgc 1560  
 ctgcgagtgc tgcacctgtc ctacaacaag ctggacctgt accatgggcg ctcgttcacg 1620  
 gagctgccgc agctggaggc actggacctc agctacaaca gccagccctt cagcatgcag 1680  
 ggcgtagggc acaacctcag ctctgtggcc cagctgccgt ccctgcgcta cctcagcctt 1740  
 gcgcacaacg gcatccacag ccgctgtgtc cagaagctca gcagcgctc gctgcgcgcc 1800  
 ctggacttca ggggcaactc cctgagccag atgtgggccc agggagacct ctatctctgc 1860  
 ttcttcaaag gcttgaggaa cctgggtccag ctggacctgt ccaagaacca cctgcacacc 1920  
 ctctgcctc gtcacctgga taacctgccc aagagcctgc gccagctgcg tctccgggac 1980  
 aataacctgg ccttcttcaa ctggagcagc ctgactgttc tgccccagct ggaagccctg 2040  
 gatctggcgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcaccggg 2100  
 ctccagaagc tggacgtgag cagcaacagc atcggtttg tgacccttg cttctttgtc 2160  
 cttgccaaac ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220  
 ttctggttcg gtcgcttaac agagaccctg aatatactag acgtgagcgc caaccgctc 2280  
 cactgtgcct gcggggcggc ctttgtggac ttctgtctgg agatgcaggc ggccgtgcct 2340  
 gggctgtcca ggcgcgtcac gtgtggcagt ccggggccagc tccagggccg cagcatcttc 2400  
 gcacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 21  
 <211> 1032  
 <212> PRT  
 <213> Canis familiaris

<400> 21

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro

545	550	555	560
Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu	565	570	575
Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg	580	585	590
Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser	595	600	605
Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg	610	615	620
Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn	625	630	635
Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser	645	650	655
Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp	660	665	670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly	675	680	685
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln	690	695	700
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro	705	710	715
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala	725	730	735
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly	740	745	750
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys	755	760	765
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro	770	775	780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly  
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu  
 805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Leu Ala Val Ala Leu Ser Leu  
 820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys  
 835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly  
 850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
 865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu  
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
 900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
 915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser  
 930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
 995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala  
1025 1030

<210> 22  
<211> 822  
<212> PRT  
<213> Canis familiaris  
  
<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu  
115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe  
 290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu  
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu  
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu  
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu  
 420 425 430



Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val  
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly  
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp  
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg  
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln  
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu  
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr  
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro  
 545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu  
 565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg  
 580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser  
 595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg  
 610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn  
 625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser  
 645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660                      665                      670  
 Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly  
       675                      680                      685  
 Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln  
       690                      695                      700  
 Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro  
 705                      710                      715                      720  
 Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala  
                     725                      730                      735  
 Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly  
                     740                      745                      750  
 Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys  
                     755                      760                      765  
 Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro  
                     770                      775                      780  
 Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly  
 785                      790                      795                      800  
 Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu  
                     805                      810                      815  
 Ser Trp Val Cys Phe Ser  
                     820

<210> 23  
 <211> 3334  
 <212> DNA  
 <213> Canis familiaris

<400> 23  
 aggaaggggc tgtgagctcc aagcatcctt tcctgcagct gctgcccagc ctgccagcca 60  
 gaccctctgg agaagcccc gtcacctgtc atgggcccct gccgtggcgc cctgcacccc 120  
 ctgtctctcc tgggtgcaggc tgccgcgcta gccctggccc tggcccaggg caccctgcct 180  
 gccttctctgc cctgtgagct ccagccccat ggctgtgtga actgcaactg gctgttcttc 240  
 aagtccgtgc cccgcttctc ggcagctgca ccccgcggtg acgtcaccag cctttccttg 300

tactccaacc gcatccacca cctccatgac tatgactttg tccacttcgt ccacctgcgg	360
cgtctcaatc tcaagtggaa ctgcccggcc gccagcctca gcccacatgca ctttcctgt	420
cacatgacca ttgagcccaa caccttcctg gctgtgcca cctagagga cctgaatctg	480
agctataaca gcatcacgac tgtgcccggc ctgcccagtt cgcttggtgc cctgtccctg	540
agccgcacca acatcctggt gctggaccct gccaccctgg caggccttta tgccctgcgc	600
ttcctgttcc tggatggcaa ctgctactac aagaaccctt gccagcaggc cctgcagggtg	660
gccccagggtg ccctcctggg cctgggcaac ctcacacacc tgtcactcaa gtacaacaac	720
ctcaccgtgg tgccgcgggg cctgcccccc agcctggagt acctgctctt gtccataaac	780
cacatcatca ccctggcacc tgaggacctg gccaatctga ctgccctgcg tgtcctcgat	840
gtgggtggga actgtcgccg ctgtgaccat gcccgtaacc cctgcaggga gtgccccaaag	900
ggcttcccc agctgcaccc caacaccttc ggccacctga gccacctga aggcctgggtg	960
ttgagggaca gctctctcta cagcctggac cccagggtgt tccatggcct gggcaacctc	1020
atggtgctgg acctgagtga gaacttcctg tatgactgca tcacaaaaac caaagccttc	1080
tacggcctgg cccggctgcg cagactcaac ctgtccttca attatcataa gaagggtgtc	1140
tttgcccacc tgcactctggc atcctccttc gggagcctac tgtccctgca ggagctggac	1200
atacatggca tcttcttccg ctgctcagc aagaccacgc tccagtcgct ggcccacctg	1260
cccatgctcc agcgtctgca tctgcagttg aactttatca gccaggccca gctcagcatc	1320
ttcgggcctt tccctggact gcggtacgtg gacttgctag acaaccgcat cagtggagct	1380
gcagagcccg cggctgccac aggggaggta gaggcagact gtggggagag agtctggcca	1440
cagtcccggt accttgctct gggcccactg ggcacccccg gctcagaggc cttcatgccc	1500
agctgcagga ccctcaactt caccttggac ctgtctcgga acaacctagt gactgttcag	1560
ccggagatgt ttgtccggtt ggcgcgcctc cagtgcctgg gcctgagcca caacagcatc	1620
tcgcaggcgg tcaatggctc gcagttcgtg cctctgagca acctgcgggt gctggacctg	1680
tcccataaca agctggacct gtaccacggg cgctcggtca cggagctgcc gcggctggag	1740
gccttggaac tcagctacaa cagccagccc ttcagcatgc ggggcgtggg ccacaatctc	1800
agctttgtgg cacagctgcc agccctgcgc tacctcagcc tggcgacaaa tggcatccac	1860
agccgcgtgt cccagcagct ccgcagcgcc tcgctccggg ccctggactt cagtggcaat	1920
accctgagcc agatgtgggc cgaggagac ctctatctcc gcttcttcca aggcctgaga	1980
agcctgggtc agctggacct gtcccagaat cgctgcata ccctcctgcc acgcaacctg	2040
gacaacctcc ccaagagcct gcggctcctg cggtccgtg acaattacct ggctttcttc	2100

aactggagca gcctggccct cctacccaag ctggaagccc tggacctggc gggaaaccag 2160  
ctgaaggccc tgagcaatgg cagcttgccc aacggcacc agctccagag gctggacctc 2220  
agcggcaaca gcatcggtt cgtggtcccc agcttttttg ccctggccgt gaggttcga 2280  
gagctcaacc tcagcgcaa cgccctcaag acggtggagc cctcctgggt tggttccctg 2340  
gcggtgccc tgaaagtct agacgtgacc gccaaccctc tgcattgcgc ttgcggcgca 2400  
accttcgtgg acttcttgct ggaggtgcag gctgcggtgc ccggcctgcc tagccgtgtc 2460  
aagtgcggca gcccgggcca gctccagggc cgcagcatct tcgcacagga cctgcgcctc 2520  
tgcctggacg aagcgtctc ctgggtctgt ttcagcctct cgctgctggc tgtggccctg 2580  
agcctggctg tgcccatgct gcaccagctc tgtggctggg acctctggta ctgctccac 2640  
ctgtgcctgg cctggctgcc ccggcggggg cgggcgggg gtgtggatgc cctggcctat 2700  
gacgccttcg tggctctga caaggcgag agctcgggtg cggactgggt gtacaatgag 2760  
ctgcgggtac agctagagga ggcgcgtggg cgccgggcgc tacgcctgtg tctggaggaa 2820  
cgtgactggg taccggcaa aacctcttc gagaacctct gggcctcagt ttacagcagc 2880  
cgcaagacgc tgtttgtgct ggccgcacg gacagagtca ggggcctcct gcgtgccagc 2940  
ttcctgctgg cccaacagcg cctgctggag gaccgcaagg acgtcgtggt gctggtgatc 3000  
ctgtgccccg acgcccaccg ctcccgctat gtgcggctgc gccagcgcct ctgccgccag 3060  
agtgtcctcc tctggcccca ccagccagt ggccagcgca gcttctgggc ccagctgggc 3120  
acggccctga ccagggacaa ccgccacttc tacaaccaga acttctgccg gggccccacg 3180  
acagcctgat aggcagacag ccagcacct tcgcgccct acacctgcc tgtctgtctg 3240  
ggatgccga cctgctggct ctacaccgcc gctctgtctc ccctacacc agccctggca 3300  
taaagcgacc gctcaataaa tgctgctggg agac 3334

&lt;210&gt; 24

&lt;211&gt; 2466

&lt;212&gt; DNA

<213> *Canis familiaris*

&lt;400&gt; 24

atgggcccct gccgtggcgc cctgcacccc ctgtctctcc tgggtcaggc tgccgcgcta 60  
gccctggccc tggcccaggg caccctgcct gccttctgc cctgtgagct ccagcccat 120  
ggcctggtga actgcaactg gctgttctc aagtccgtgc ccgcttctc ggcagctgca 180  
ccccgcggtg acgtcaccag ctttctcttg tactccaacc gcatccacca cctccatgac 240  
tatgactttg tccacttcgt ccacctgcgg cgtctcaatc tcaagtggaa ctgcccggcc 300

gccagcctca gccccatgca ctttccctgt cacatgacca ttgagcccaa caccttcctg 360  
 gctgtgccca ccctagagga cctgaatctg agctataaca gcatcacgac tgtgcccgcc 420  
 ctgcccagtt cgcttgtgtc cctgtccctg agccgcacca acatcctggg gctggaccct 480  
 gccaccctgg caggccttta tgccctgcmc ttctgttcc tggatggcaa ctgctactac 540  
 aagaaccctt gccagcaggc cctgcagggt gcccagggt ccctcctggg cctgggcaac 600  
 ctcacacacc tgtcactcaa gtacaacaac ctcaccgtgg tgccgcgggg cctgcccccc 660  
 agcctggagt acctgctctt gtctacaac cacatcatca ccctggcacc tgaggacctg 720  
 gccaatctga ctgccctgcm tgtcctcgat gtgggtggga actgtcgccg ctgtgaccat 780  
 gcccgttaacc cctgcaggga gtgccccaa ggttcccc agctgcaccc caacaccttc 840  
 ggccacctga gccacctoga aggcctgggt ttgagggaca gctctctcta cagcctggac 900  
 cccagggtgt tccatggcct gggcaacctc atgggtgctg acctgagtga gaacttcctg 960  
 tatgactgca tcacaaaaac caaagccttc tacggcctgg ccgggtgcm cagactcaac 1020  
 ctgtccttca attatcataa gaagggtgct ttgcccacc tgcactgcm atcctccttc 1080  
 gggagcctac tgtccctgca ggagctggac atacatggca tcttcttccg ctgctcagc 1140  
 aagaccacgc tccagtcgct ggccacctg cccatgctcc agcgtctgca tctgcagttg 1200  
 aactttatca gccaggccca gctcagcatc ttgggcgctt tccctggact gcggtacgtg 1260  
 gacttgtcag acaaccgcat cagtggagct gcagagcccg cggctgccac aggggaggtg 1320  
 gaggcagact gtggggagag agtctggcca cagtcccggt accttgctct gggccactg 1380  
 ggcaaccccg gctcagagga cttcatgcm agctgcagga ccctcaactt caccttgga 1440  
 ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggt ggcgcgcctc 1500  
 cagtgcctgg gcctgagcca caacagcatc tcgcaggcm tcaatggctc gcagttcgtg 1560  
 cctctgagca acctgcgggt gctggacctg tcccataaca agctggacct gtaccacggg 1620  
 cgctcgttca cggagctgcm gcggctggag gccttggaac tcagctacaa cagccagccc 1680  
 ttcagcatgc ggggcgtggg ccacaatctc agctttgtgg cacagctgcm agccctgcmc 1740  
 tacctcagcc tggcgcacaa tggcatccac agccgcgtgt cccagcagct ccgcagcm 1800  
 tcgctccggg ccctggactt cagtggcaat accctgagcm agatgtgggc cgaggagac 1860  
 ctctatctcc gcttcttcca aggcctgaga agcctggctt agctggacct gtcccagaat 1920  
 cgctgcata ccctcctgcm acgcaacctg gacaacctc ccaagagcct gcggtcctg 1980  
 cggctccgtg acaattacct ggctttcttc aactggagca gcctggccct cctaccaag 2040

```

ctggaagccc tggacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100
aacggcacccc agctccagag gctggacctc agcggcaaca gcatcggtt cgtgggtcccc 2160
agcttttttg ccctggcgtt gaggtttcga gagctcaacc tcagcgccaa cgccctcaag 2220
acgggtggagc cctcctgggt tggttccctg gcgggtgccc tgaaagtcct agacgtgacc 2280
gccaaaccctt tgcattgcgc ttgcggcgca accttcgtgg acttcttgct ggaggtgcag 2340
gctgcggtgc ccggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccagggc 2400
cgcagcatct tcgcacagga cctgcgcctc tgctgggacg aagcgtcttc ctgggtctgt 2460
ttcagc 2466

```

```

<210> 25
<211> 1031
<212> PRT
<213> Felis catus

```

```

<400> 25

```

```

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1           5           10           15

```

```

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
          20           25           30

```

```

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
          35           40           45

```

```

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
          50           55           60

```

```

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65           70           75           80

```

```

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
          85           90           95

```

```

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
          100          105          110

```

```

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
          115          120          125

```

```

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
          130          135          140

```

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe



610	615	620
Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635 640
His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg		
	645	650 655
Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser		
	660	665 670
Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln		
	675	680 685
Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln		
	690	695 700
Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe		
	705	710 715 720
Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala		
	725	730 735
Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu		
	740	745 750
Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala		
	755	760 765
Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu		
	770	775 780
Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser		
	785	790 795 800
Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp		
	805	810 815
Asp Cys Phe Gly Leu Ser Leu Leu Thr Val Ala Leu Gly Leu Ala Val		
	820	825 830
Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His		
	835	840 845

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Gly Ala Asp  
 850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala  
 865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg  
 885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu  
 900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser  
 915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu  
 930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg  
 945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser  
 965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu  
 980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly  
 995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe  
 1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu  
 1025 1030

<210> 26

<211> 820

<212> PRT

<213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn  
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met  
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser  
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro  
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe  
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe  
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu  
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala  
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu  
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu  
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu  
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu  
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser  
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser  
 485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val  
 500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu  
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu  
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser  
 545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala  
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
 610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg  
 645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser  
 660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln  
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln  
 690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe  
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

<210> 27  
<211> 3235  
<212> DNA  
<213> *Felis catus*

<400> 27  
aggggtctgcg agctccaggc attcttctct gccatcgctg cccagtctgc catccagacc 60  
ctctggagaa gccccactc cctgtcatgg gcccctgcc tggcgccctg cccccctgt 120  
ctctcctggg gcaggctgcc gcgctggccg tggccctggc ccagggcacc ctgcctgcct 180  
ttctgccctg tgagctccag cgccacggcc tgggtgaattg cgactggctg ttctcaagt 240  
cgtgccccca cttctcggcg gcagcgcccc gtggtaacgt caccagcctt tccctgtact 300  
ccaaccgcat ccaccacctc cactgactccg actttgtcca cctgtccagc ctgcgggcgtc 360  
tcaacctcaa atggaactgc ccaccgccca gcctcagccc catgcacttc ccctgtcaca 420  
tgaccattga gccccacacc ttcttgggcg tgcccaccct ggaggagctg aacctgagct 480  
acaacagcat cactgacagta ccgcccctgc ccagttccct cgtgtccctg tccttgagcc 540  
gtaccaacat cctgggtgctg gaccctgcc aacctgcagg gctgcactcc ctgcgctttc 600  
tgttcttgga tggcaactgc tactacaaga acccctgccc gcaggccctg caggtggccc 660  
cgggcgccct ccttggcctg ggcaacctta cgcacctgtc actcaagtac aacaacctca 720  
ctgcggtgcc ccgcggcctg cccccagcc tggagtacct gctattgtcc tacaaccaca 780

tcataccacct	ggcacctgag	gacctggcca	acctgaccgc	cctgcgtgtg	ctcgatgtgg	840
gtgggaactg	ccgtcgctgt	gaccacgccc	gcaaccctg	tatggagtgc	cccaagggtc	900
tcccgcacct	gcacctgac	accttcagcc	acctgaacca	cctcgaaggc	ctgggtgtga	960
aggacagctc	tctctacaac	ctgaacccca	gatggttcca	tgccctgggc	aacctcatgg	1020
tgctggacct	gagtgagaac	ttcctatatg	actgcatcac	caaaaccaca	gccttccagg	1080
gcctggccca	gctgcgcaga	ctcaacttgt	ctttcaatta	ccacaagaag	gtgtcctttg	1140
cccacctgca	tctggcgccc	tccttcggga	gcctgctctc	cctgcagcag	ctggacatgc	1200
atggcatctt	cttcgcgtcg	ctcagcgaga	ccacgctccg	gtcgcgtggc	cacctgcccc	1260
tgctccagag	tctgcacctg	cagatgaact	tcataaatca	ggcccagctc	agcatcttcg	1320
gggccttccc	tggcctgcga	tacgtggacc	tgtcagacaa	ccgcataagt	ggagccatgg	1380
agctggcggc	tgccacgggg	gaggtggatg	gtggggagag	agtccggctg	ccatctgggg	1440
acctagctct	ggccccaccg	ggcaccccta	gctccgaggg	cttcatgcca	ggctgcaaga	1500
ccctcaactt	caccttggac	ctgtcacgga	acaacctagt	gacaatccag	ccagagatgt	1560
ttgcccggct	ctcgcgctc	cagtgcctgc	tcctgagccg	caacagcatc	tcgcaggcag	1620
tcaacggctc	acaatttatg	ccgctgacca	gcctgcaggt	gctggacctg	tcccataaca	1680
agctggacct	gtaccatggg	cgctctttca	cggagctgcc	gcggctggag	gccctggacc	1740
tcagctacaa	cagccagccc	ttcagcatgc	agggcgtggg	tcacaacctc	agctttgtgg	1800
cacagctgcc	ggccctgcgc	tatctcagcc	tggcgcacaa	cgacatccac	agccgtgtgt	1860
cccagcagct	ctgcagcgcc	tcgctgcggg	ccttggactt	cagcggcaat	gccttgagcc	1920
ggatgtgggc	cgaggagagc	ctgtatctcc	acttcttccg	aggcctgagg	agcctggtcc	1980
ggttggatct	gtcccagaat	cgccctgata	ccctcttgcc	acgcaccctg	gacaacctcc	2040
ccaagagcct	gcggctgctg	cgtctccgtg	acaattatct	ggctttcttc	aactggagca	2100
gcctggtcct	cctccccagg	ctggaagccc	tggacctggc	gggaaaccag	ctgaaggccc	2160
tgagcaacgg	cagcttgcc	aatggaaccc	agctccagag	gctggacctc	agcagcaaca	2220
gtatcagctt	cgtggcctcc	agcttttttg	ctctggccac	caggctgcga	gagctcaacc	2280
tcagtgcaca	cgccctcaag	acggtggagc	cctcctgggt	cggttctcta	gcgggcaccc	2340
tgaagtcct	agatgtgact	ggcaaccccc	tgcactgcgc	ctgtggggcg	gccttcgtgg	2400
acttcttgct	ggaggtgcag	gctgcagtgc	ccggcctgcc	aggccacgct	aagtgtggca	2460
gtccaggtea	gctccagggc	cgcagcatct	ttgcgcagga	tctgcgcctc	tgccctggatg	2520
aggccctctc	ctgggactgt	tttggcctct	cgctgctgac	cgtggccctg	ggcctggccg	2580

tgcccatgct gcaccacctc tgtggctggg acctctggta ctgcttcac ctgtgcctgg 2640  
 cctggctgcc ccggcggggg cggcggcggg gcgcggatgc cctgccctac gatgcctttg 2700  
 tggctcttca caaggcacag agcgcggtgg ccgactgggt gtacaacgag ctgcgggtac 2760  
 ggctagagga gcgccgtgga cgcgcgagcg tccgcctgtg cctggaggaa cgtgactggc 2820  
 taccgggtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc 2880  
 tgtttgtgct ggcccacaca gacaggggtca gggcctctt gcgcgccagc tttctgctgg 2940  
 cccagcagcg cctgtggag gaccgcaagg acgttgtggg gctgggtgatc ctgcgccccg 3000  
 acgcccaccg cttccgctat gtgcggctgc gccagcgct ctgccgccag agcgtcctcc 3060  
 tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc acggccctga 3120  
 ccagggacaa ccagcacttc tataaccaga acttctgccg gggcccccacg acggcagagt 3180  
 gaccgcccag caccccaagc ctccctacacc ttgcctgtct gcctgggatg ccggg 3235

<210> 28

<211> 2460

<212> DNA

<213> Felis catus

<400> 28

atggggccct gccatggcgc cctgcacccc ctgtctctcc tggcgcaggc tgccgcgctg 60  
 gccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgccac 120  
 ggcctgggta attgcgactg gctgttcctc aagtccgtgc ccacttctc ggcggcagcg 180  
 ccccgctggta acgtcaccag cctttccctg tactccaacc gcattccacca cctccacgac 240  
 tccgactttg tccacctgtc cagcctgcgg cgtctcaacc tcaaattggaa ctgccacccc 300  
 gccagcctca gcccctatgca cttcccctgt cacatgacca ttgagcccca caccttctctg 360  
 gccgtgcca ccctggagga gctgaacctg agctacaaca gcattcacgac agtaccgccc 420  
 ctgccagtt ccctcgtgtc cctgtccttg agcgtacca acatcctggg gctggaccct 480  
 gccaacctcg cagggtgca ctccctgcgc tttctgttcc tggatggcaa ctgtactac 540  
 aagaaccctt gccgcaggc cctgcagggt gcccggggcg cctccttg cctgggcaac 600  
 cttacgcacc tgtcactcaa gtacaacaac ctactgcgg tgccccgcgg cctgcccccc 660  
 agcctggagt acctgctatt gtccataaac cacatcatca ccctggcacc tgaggacctg 720  
 gccaacctga ccgcctgcg tgtgtctgat gtgggtggga actgccgtcg ctgtgaccac 780  
 gccgcgaacc cctgtatgga gtgcccgaag ggcttccgc acctgcaccc tgacaccttc 840  
 agccacctga accacctga aggcctgggt ttgaaggaca gctctctcta caacctgaac 900



```

cccagatggg tccatgccct gggcaacctc atgggtgctgg acctgagtga gaacttccta 960
tatgactgca tcaccaaaac cacagccttc cagggcctgg cccagctgcg cagactcaac 1020
ttgtctttca attaccacaa gaaggtgtcc ttgcccacc tgcattctggc gccctccttc 1080
gggagcctgc tctccctgca gcagctggac atgcatggca tcttcttccg ctgctcagc 1140
gagaccacgc tccggctcgt ggtccacctg cccatgctcc agagtctgca cctgcagatg 1200
aacttcatca atcaggccca gctcagcatc ttcggggcct tccctggcct gcgatacgtg 1260
gacctgtcag acaaccgcat aagtggagcc atggagctgg cggtgccac gggggaggtg 1320
gatggtgggg agagagtccg gctgccatct ggggacctag ctctggggcc accgggcacc 1380
cctagctccg agggcttcat gccaggctgc aagaccctca acttcacctt ggacctgtca 1440
cggaacaacc tagtgacaat ccagccagag atgtttgccc ggctctcgcg cctccagtgc 1500
ctgctcctga gccgcaacag catctcgcag gcagtcaacg gctcacaatt tatgccgctg 1560
accagcctgc aggtgctgga cctgtcccat aacaagctgg acctgtacca tgggcgctct 1620
ttcacggagc tgcccgggct ggaggccctg gacctcagct acaacagcca gcccttcagc 1680
atgcagggcg tgggtcacia cctcagcttt gtggcacagc tgccggccct gcgctatctc 1740
agcctggcgc acaacgacat ccacagccgt gtgtcccagc agctctgcag cgcctcgtg 1800
cgggccttgg acttcagcgg caatgccttg agccggatgt gggccgaggg agacctgtat 1860
ctccacttct tccgaggcct gaggagcctg gtccggtttg atctgtcca gaatcgctg 1920
cataccctct tgccacgcac cctggacaac ctcccaaga gcctgcggct gctgcgtctc 1980
cgtgacaatt atctggcttt cttcaactgg agcagcctgg tcctcctccc caggctggaa 2040
gccctggacc tggcgggaaa ccagctgaag gccctgagca acggcagctt gcctaattga 2100
accagctcc agaggctgga cctcagcagc aacagtatca gcttcgtggc ctccagcttt 2160
tttgctctgg ccaccaggct gcgagagctc aacctcagtg ccaacgccct caagacgggtg 2220
gagccctcct ggttcgggtc tctagcgggc accctgaaag tcctagatgt gactggcaac 2280
cccctgcact gcgcctgtgg ggcggccttc gtggacttct tgctggaggt gcaggctgca 2340
gtgcccgcc tgccaggcca cgtcaagtgt ggcagtccag gtcagctcca gggccgcagc 2400
atctttgcgc aggatctgcg cctctgcctg gatgaggccc tctcctggga ctgttttggc 2460

```

&lt;210&gt; 29

&lt;211&gt; 1032

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225	230	235	240
Ala Asn Leu Thr	Ser Leu Arg Val Leu Asp	Val Gly Gly Asn Cys Arg	
	245	250	255
Arg Cys Asp His	Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser		
	260	265	270
Leu His Leu His	Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly		
	275	280	285
Leu Val Leu Lys Asp	Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe		
	290	295	300
Gln Gly Leu Val	Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu		
305	310	315	320
Tyr Glu Ser Ile	Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu		
	325	330	335
Arg Lys Leu Asn	Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala		
	340	345	350
Arg Leu His Leu	Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu		
	355	360	365
Leu Asn Met Asn	Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu		
	370	375	380
Arg Trp Leu Ala	Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met		
385	390	395	400
Asn Phe Ile Asn	Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala		
	405	410	415
Leu Arg Phe Val	Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr		
	420	425	430
Leu Ser Glu Ala	Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu		
	435	440	445
Leu Leu Ser Ala	Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser		
	450	455	460

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu  
 465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu  
 485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala  
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp  
 515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu  
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe  
 545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser  
 565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val  
820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe  
835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser  
850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu  
885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp  
900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His  
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
 980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln  
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln  
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu  
 1025 1030

<210> 30  
 <211> 821  
 <212> PRT  
 <213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln  
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu  
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn  
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn  
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp  
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met  
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu  
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser  
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala  
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly  
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro  
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr  
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser  
 260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe  
 290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340	345	350
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu		
355	360	365
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu		
370	375	380
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met		
385	390	395
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala		
405	410	415
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr		
420	425	430
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu		
435	440	445
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser		
450	455	460
Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu		
465	470	475
Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu		
485	490	495
Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala		
500	505	510
Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp		
515	520	525
Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu		
530	535	540
Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe		
545	550	555
Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser		
565	570	575



Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val  
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly  
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe  
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn  
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu  
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr  
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn  
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu  
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala  
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn  
 725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn  
 740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly  
 755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly  
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg  
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser  
 805 810 815

Trp Asp Cys Phe Gly  
820

<210> 31

<211> 3200

<212> DNA

<213> Mus musculus

<400> 31

```

tgtcagaggg agcctcggga gaatcctcca tctcccaaca tggttctccg tcgaaggact    60
ctgcacccct tgtccctcct ggtacaggct gcagtgtctg ctgagactct ggccctgggt    120
accctgcctg cttcctacc ctgtgagctg aagcctcatg gcctgggtgga ctgcaattgg    180
ctgttctctga agtctgtacc ccgtttctct gcggcagcat cctgctccaa catcacccgc    240
ctctccttga tctccaaccg tatccaccac ctgcacaact ccgaattcgt ccacctgtcc    300
aacctgcggc agctgaacct caagtggaac tgtccacca ctggccttag cccctgcac    360
ttctcttgcc acatgaccat tgagcccaga accttctctg ctatgcgtac actggaggag    420
ctgaacctga gctataatgg tatcaccact gtgccccgac tgcccagctc cctggtgaat    480
ctgagcctga gccacaccaa catcctgggt ctagatgcta acagcctcgc cggcctatac    540
agcctgcgcg ttctcttcat ggacgggaac tgctactaca agaaccctg cacaggagcg    600
gtgaagggtga cccagggcgc cctcctgggc ctgagcaatc tcacccatct gtctctgaag    660
tataacaacc tcacaaaggt gccccgcaa ctgccccca gcctggagta cctcctgggt    720
tcctataacc tcattgtcaa gctggggcct gaagacctgg ccaatctgac ctcccttoga    780
gtacttgatg tgggtgggaa ttgccgtcgc tgcgaccatg cccccaatcc ctgtatagaa    840
tgtggccaaa agtccctcca cctgcaccct gagaccttcc atcacctgag ccatctggaa    900
ggcctgggtgc tgaaggacag ctctctccat aactgaact cttcctgggt ccaaggtctg    960
gtcaacctct cgggtgctga cctaagcgag aactttctct atgaaagcat caaccacacc   1020
aatgcctttc agaacctaac ccgcctgcgc aagctcaacc tgtccttcaa ttaccgcaag   1080
aaggatcctt ttgccgcct ccacctggca agttccttca agaacctggg gtcactgcag   1140
gagctgaaca tgaacggcat cttcttccgc tcgctcaaca agtacacgct cagatggctg   1200
gccgatctgc caaaactcca cactctgcat cttcaaatga acttcatcaa ccaggcacag   1260
ctcagcatct ttggtacctt ccgagccctt cgctttgtgg acttgtcaga caatcgcac   1320
agtgggcctt caacgctgtc agaagccacc cctgaagagg cagatgatgc agagcaggag   1380
gagctgttgt ctgcggatcc tcacccagct ccactgagca cccctgcttc taagaacttc   1440

```

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact	1500
atcaagccag agatgtttgt caatctctca cgcctccagt gtcttagcct gagccacaac	1560
tccattgcac aggctgtcaa tggctctcag ttctgtccgc tgactaatct gcaggtgctg	1620
gacctgtccc ataacaaact ggacttgtac cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacctgag ctacaacagc cagcccttta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggccca tctgtccatg ctacacagcc ttagcctggc acacaatgac	1800
attcataccc gtgtgtcctc acatctcaac agcaactcag tgaggtttct tgacttcagc	1860
ggcaacggta tgggcccgcg gtgggatgag gggggccttt atctccattt cttccaaggc	1920
ctgagtggcc tgctgaagct ggacctgtct caaaataacc tgcataatct ccggccccag	1980
aaccttgaca acctccccaa gagcctgaag ctgtgtgagc tccgagacaa ctacctatct	2040
ttctttaact ggaccagtct gtccttctctg cccaacctgg aagtcctaga cctggcaggc	2100
aaccagctaa aggccctgac caatggcacc ctgcctaata gcaccctcct ccagaaactg	2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgctct ggcggtcgag	2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctggtttggg	2280
ccatttgtga tgaacctgac agttctagac gtgagaagca accctctgca ctgtgcctgt	2340
ggggcagcct tcgtagactt actgttggag gtgcagacca aggtgcctgg cctggctaata	2400
ggtgtgaagt gtggcagccc cggccagctg cagggcgta gcatcttcgc acaggacctg	2460
cggctgtgcc tggatgaggt cctctcttgg gactgctttg gcctttcact cttggctgtg	2520
gccgtgggca tgggtgggccc tatactgcac catctctgcg gctgggacgt ctggtactgt	2580
tttcatctgt gcctggcatg gctacctttg ctggcccgca gccgacgcag cgcccaagct	2640
ctcccctatg atgccttcgt ggtgttcgat aaggcacaga gcgcagttgc ggactgggtg	2700
tataacgagc tgccgggtgcg gctggaggag cggcgcggtc gccgagccct acgcttgtgt	2760
ctggaggacc gagattggct gcctggccag acgctcttcg agaacctctg ggcttccatc	2820
tatgggagcc gcaagactct atttgtgctg gccacacgg accgcgtcag tggcctcctg	2880
cgcaccagct tcctgctggc tcagcagcgc ctgttgggaag accgcaagga cgtgggtggg	2940
ttggtgatcc tgcgtccgga tgcccaccgc tcccgtatg tgcgactgcg ccagcgtctc	3000
tgccgccaga gtgtgctctt ctggccccag cagcccaacg ggcagggggg cttctggggc	3060
cagctgagta cagccctgac tagggacaac cgccacttct ataaccagaa cttctgccgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcatctt catgcctggg	3180
tcccagttg ctctgcctgc	3200

<210> 32  
 <211> 2463  
 <212> DNA  
 <213> Mus musculus

<400> 32  
 atggttctcc gtcgaaggac tctgcacccc ttgtccctcc tggtagaggc tgcagtgtcg 60  
 gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120  
 ggctggtgg actgcaattg gctgttcctg aagtctgtac ccggtttctc tgcggcagca 180  
 tctgtctcca acatcacccg cctctccttg atctccaacc gtatccacca cctgcacaac 240  
 tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300  
 actggcctta gccccctgca cttctcttgc cacatgacca ttgagcccag aaccttcctg 360  
 gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420  
 ctgcccagct ccctggtgaa tctgagcctg agccacacca acatcctggt tctagatgct 480  
 aacagcctcg ccggcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540  
 aagaacccct gcacaggagc ggtgaagggtg accccaggcg ccctcctggg cctgagcaat 600  
 ctcacccatc tgtctctgaa gtataacaac ctcacaaagg tgccccgcca actgcccccc 660  
 agcctggagt acctcctggt gtcctataac ctcatgttca agctggggcc tgaagacctg 720  
 gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgaccat 780  
 gcccccaatc cctgtataga atgtggccaa aagtcctcc acctgcaccc tgagaccttc 840  
 catcacctga gccatctgga aggcctgggt ctgaaggaca gctctctcca tacactgaac 900  
 tcttcctggt tccaaggctc ggtcaacctc tcggtgctgg acctaagcga gaactttctc 960  
 tatgaaagca tcaaccacac caatgccttt cagaacctaa cccgcctgcg caagctcaac 1020  
 ctgtccttca attaccgcaa gaaggtatcc tttgcccgcc tccacctggc aagttccttc 1080  
 aagaacctgg tgtcactgca ggagctgaac atgaacggca tcttcttccg ctcgctcaac 1140  
 aagtacacgc tcagatggct ggccgatctg cccaaactcc acactctgca tcttcaaagt 1200  
 aacttcacat accaggcaca gctcagcatc tttggtacct tccgagccct tcgctttgtg 1260  
 gacttgctcag acaatcgcat cagtgggcct tcaacgctgt cagaagccac ccctgaagag 1320  
 gcagatgatg cagagcagga ggagctgttg tctgcggatc ctcaccacgc tccactgagc 1380  
 acccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440  
 tctcggaaca acctggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500  
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctgccg 1560

```

ctgactaatc tgcaggtgct ggacctgtcc cataacaaac tggacttgta ccactggaaa 1620
tcgttcagtg agctaccaca gttgcaggcc ctggacctga gctacaacag ccagcccttt 1680
agcatgaagg gtataggcca caatttcagt tttgtggccc atctgtccat gctacacagc 1740
cttagcctgg cacacaatga cattcatacc cgtgtgtcct cacatctcaa cagcaactca 1800
gtgagggtttc ttgacttcag cggcaacggg atgggcccga tgtgggatga ggggggcctt 1860
tatctccatt tcttccaagg cctgagtggc ctgctgaagc tggacctgtc tcaaaataac 1920
ctgcatatcc tccggcccca gaaccttgac aacctcccca agagcctgaa gctgctgagc 1980
ctccgagaca actacctatc tttctttaac tggaccagtc tgtccttctt gcccaacctg 2040
gaagtccatg acctggcagg caaccagcta aaggccctga ccaatggcac cctgcctaata 2100
ggcacccctcc tccagaaact ggatgtcagc agcaacagta tcgtctctgt ggtcccagcc 2160
ttcttcgctc tggcggtcga gctgaaagag gtcaacctca gccacaacat tctcaagacg 2220
gtggatcgct cctggtttgg gccatttgat atgaacctga cagttctaga cgtgagaagc 2280
aaccctctgc actgtgcctg tggggcagcc ttcgtagact tactgttgga ggtgcagacc 2340
aagggtgctg gcctggctaa tgggtgtgaag tgtggcagcc ccggccagct gcagggccgt 2400
agcatcttcg cacaggacct gcggctgtgc ctggatgagg tcctctcttg ggactgcttt 2460
ggc 2463

```

```

<210> 33
<211> 1032
<212> PRT
<213> Homo sapiens

```

```

<400> 33

```

```

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1           5           10           15

```

```

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20           25           30

```

```

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35           40           45

```

```

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50           55           60

```

```

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65           70           75           80

```

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp  
                     85                                    90                                    95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met  
                     100                                    105                                    110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
                     115                                    120                                    125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser  
                     130                                    135                                    140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser  
 145                                    150                                    155                                    160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly  
                     165                                    170                                    175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro  
                     180                                    185                                    190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
                     195                                    200                                    205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr  
                     210                                    215                                    220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu  
 225                                    230                                    235                                    240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
                     245                                    250                                    255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe  
                     260                                    265                                    270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
                     275                                    280                                    285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe  
                     290                                    295                                    300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu

305		310		315		320
Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu						
	325			330		335
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala						
	340			345		350
His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu						
	355			360		365
Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu						
	370			375		380
Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met						
	385			390		395
						400
Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly						
		405		410		415
Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu						
	420			425		430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu						
	435			440		445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu						
	450			455		460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser						
	465			470		475
						480
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser						
	485			490		495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val						
	500			505		510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu						
	515			520		525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu						
	530			535		540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly  
 545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr  
 565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser  
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
 595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
 610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu  
 625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln  
 645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
 660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
 675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
 690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
 705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
 725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
 740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
 755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
 770 775 780



Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val  
820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His  
835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp  
850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln  
865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu  
885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp  
900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr  
915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser  
930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu  
945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg  
965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val  
980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln  
995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg  
1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu  
1025 1030

<210> 34  
<211> 820  
<212> PRT  
<213> Homo sapiens  
  
<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln  
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe  
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu  
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn  
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp  
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp  
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met  
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu  
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser  
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser  
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly  
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro  
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr  
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr  
 210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu  
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg  
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe  
 260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly  
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe  
 290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu  
 305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu  
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala  
 340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu  
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu  
 370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met  
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly  
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420                                      425                                      430  
 Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu  
           435                                      440                                      445  
  
 Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu  
           450                                      455                                      460  
  
 Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser  
           465                                      470                                      475                                      480  
  
 Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser  
                                     485                                      490                                      495  
  
 His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val  
                                     500                                      505                                      510  
  
 Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu  
                                     515                                      520                                      525  
  
 Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu  
                                     530                                      535                                      540  
  
 Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly  
                                     545                                      550                                      555                                      560  
  
 Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr  
                                     565                                      570                                      575  
  
 Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser  
                                     580                                      585                                      590  
  
 Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn  
                                     595                                      600                                      605  
  
 Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe  
                                     610                                      615                                      620  
  
 Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu  
                                     625                                      630                                      635                                      640  
  
 His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln  
                                     645                                      650                                      655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser  
660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg  
675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg  
690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe  
705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala  
725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu  
740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala  
755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu  
770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser  
785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp  
805 810 815

Asp Cys Phe Ala  
820

<210> 35

<211> 3352

<212> DNA

<213> Homo sapiens

<400> 35

aggctggtat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtgggaag 60

ggacctcgag tgtgaagcat ccttcctgt agctgctgtc cagtctgccc gccagacct 120

ctggagaagc cctgcccc cagcatgggt ttctgccgca gcgccctgca cccgctgtct 180

ctcctgggtgc aggccatcat gctggccatg accctggccc tgggtacctt gctgccttc 240

ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

gtgccccact tctccatggc agcaccocgt ggcaatgtca ccagcctttc cttgtcctcc 360  
 aaccgcatcc accacctcca tgattctgac tttgccaccc tgcccagcct gcggcatctc 420  
 aacctcaagt ggaactgccc gccggttggc ctcagcccca tgcacttccc ctgccacatg 480  
 accatcgagc ccagcacott cttggtgtg cccaccctgg aagagctaaa cctgagctac 540  
 aacaacatca tgactgtgcc tgcgtgccc aaatccctca tatccctgtc cctcagccat 600  
 accaacatcc tgatgctaga ctctgccagc ctgcgggcc tgcattgccct gcgcttccca 660  
 ttcattggacg gcaactgtta ttacaagaac ccctgcaggc aggcactgga ggtggccccg 720  
 ggtgccctcc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact 780  
 gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tgttgcctca caaccgcatc 840  
 gtcaaaactgg cgcttgagga cctggccaat ctgaccgccc tgcgtgtgct cgatgtgggc 900  
 ggaaattgcc gccgctgcga ccacgctccc aaccctgca tggagtggcc tcgtcacttc 960  
 cccagctac atcccgatac cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag 1020  
 gacagttctc tctcctggct gaatgccagt tgggtccgtg ggctgggaaa cctccgagtg 1080  
 ctggacctga gtgagaactt cctctacaaa tgcattacta aaaccaaggc cttccagggc 1140  
 ctaacacagc tgcgcaagct taacctgtcc ttcaattacc aaaagagggt gtcctttgcc 1200  
 cacctgtctc tggccccctc cttcgggagc ctggtcgccc tgaaggagct ggacatgcac 1260  
 ggcatcttct tccgctcact cgatgagacc acgctccggc cactggcccc cctgcccattg 1320  
 ctccagactc tgcgtctgca gatgaacttc atcaaccagg cccagctcgg catcttcagg 1380  
 gccttccctg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag 1440  
 ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggctgca gcctggggac 1500  
 cttgtctcgg cccagtgga cactcccagc tctgaagact tcaggcccaa ctgcagcacc 1560  
 ctcaacttca ccttggtatc gtcacggaac aacctggtga ccgtgcagcc ggagatgttt 1620  
 gccagctct cgcacctgca gtgcctgcgc ctgagccaca actgcatctc gcaggcagtc 1680  
 aatggctccc agttcctgcc gctgaccggc ctgcaggtgc tagacctgtc ccgcaataag 1740  
 ctggacctct accacgagca ctcatcacc gagctaccgc gactggaggc cctggacctc 1800  
 agctacaaca gccagccctt tggcatgcag ggcgtggggc acaacttcag cttcgtggct 1860  
 cacctgcgca ccctgcgcca cctcagcctg gccacaaca acatccacag ccaagtgtcc 1920  
 cagcagctct gcagtacgtc gctgcggggc ctggacttca gcggcaatgc actgggccat 1980  
 atgtggggcg agggagacct ctatctgcac ttcttccaag gcctgagcgg tttgatctgg 2040

ctggacttgt cccagaaccg cctgcacacc ctctgcccc aaacctgcg caacctcccc 2100  
 aagagcctac aggtgctgcg tctccgtgac aattacctgg ccttctttaa gtggtggagc 2160  
 ctccacttcc tgcccaaact ggaagtctc gacctggcag gaaaccggct gaaggccctg 2220  
 accaatggca gcctgcctgc tggcaccgg ctccggaggc tggatgtcag ctgcaacagc 2280  
 atcagcttcg tggcccccg cttcttttcc aaggccaagg agctgcgaga gctcaacctt 2340  
 agcgccaacg ccctcaagac agtggaccac tcctggtttg ggccctggc gagtgcctg 2400  
 caaatactag atgtaagcgc caacctctg cactgcgcct gtggggcggc ctttatggac 2460  
 ttctgtctgg aggtgcagge tgccgtgcc ggtctgcca gccgggtgaa gtgtggcagt 2520  
 ccggggcagc tccagggcct cagcatcttt gcacaggacc tgcgcctctg cctggatgag 2580  
 gccctctcct gggactgttt cgccctctcg ctgctggctg tggctctggg cctgggtgtg 2640  
 cccatgctgc atcacctctg tggctgggac ctctggtact gcttccacct gtgcctggcc 2700  
 tggcttccct ggccggggcg gcaaagtgg cgagatgagg atgccctgcc ctacgatgcc 2760  
 ttctgtgtct tcgacaaaac gcagagcgca gtggcagact ggggtgtaaa cgagcttcgg 2820  
 gggcagctgg aggagtgcg tgggcgctgg gactccgcc tgtgcctgga ggaacgcgac 2880  
 tggctgcctg gcaaaaccct ctttgagaac ctgtgggcct cggctctatg cagccgcaag 2940  
 acgctgtttg tgctggccca cacggaccgg gtcagtggtc tcttgccgcg cagcttcctg 3000  
 ctggcccagc agcgctgct ggaggaccgc aaggacgtcg tgggtctggt gatcctgagc 3060  
 cctgacggcc gccgctcccg ctacgtgcgg ctgcgccagc gcctctgccg ccagagtgtc 3120  
 ctctcttggc cccaccagcc cagtggtcag cgcagcttct gggcccagct gggcatggcc 3180  
 ctgaccaggg acaaccacca cttctataac cggaacttct gccagggacc cacggccgaa 3240  
 tagccgtgag ccggaatcct gcacggtgcc acctccacac tcacctcacc tctgcctgcc 3300  
 tggcttgacc ctccctgct cgcctccctc accccacacc tgacacagag ca 3352

&lt;210&gt; 36

&lt;211&gt; 2460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

atgggtttct gccgcagcgc cctgcacccg ctgtctctcc tgggtgcaggc catcatgctg 60  
 gccatgacct tggccctggg taccttgcc gccttcctac cctgtgagct ccagccccac 120  
 ggctggtga actgcaactg gctgttctcg aagtctgtgc cccacttctc catggcagca 180  
 ccccggtggc atgtcaccag cctttccttg tcctccaacc gcatccacca cctccatgat 240

tctgactttg cccacctgcc cagcctgcgg catctcaacc tcaagtggaa ctgcccgcg 300  
gttggectca gcccacatgca cttcccctgc cacatgacca tcgagcccag caccttcttg 360  
gctgtgcccc ccttggaaga gctaaacctg agctacaaca acatcatgac tgtgcctgcg 420  
ctgccccaat cctcatatc cctgtccctc agccatacca acatcctgat gctagactct 480  
gccagcctcg cgggcctgca tgcctgcgc ttcctattca tggacggcaa ctgttattac 540  
aagaacccct gcaggcaggc actggagggtg gccccgggtg cctccttg cctgggcaac 600  
ctcaccacac tgtcactcaa gtacaacaac ctactgtgg tgcggcgaa cctgccttc 660  
agcctggagt atctgctgtt gtcctacaac cgcctgtca aactggcgcc tgaggacctg 720  
gccaatctga cggccctgcg tgtgctcgat gtggcgga attgccgcg ctgcgaccac 780  
gctcccaacc cctgcatgga gtgcctcgt cacttcccc agctacatcc cgatacctc 840  
agccacctga gccgtcttga aggcctggtg ttgaaggaca gttctctctc ctggctgaat 900  
gccagttggt tccgtgggct gggaaacctc cgagtgttg acctgagtga gaacttctc 960  
tacaaatgca tcaactaaaac caaggccttc cagggcctaa cacagctgcg caagcttaac 1020  
ctgtccttca attaccaaaa gaggggtgtcc ttgcccacc tgtctctggc ccttccttc 1080  
gggagcctgg tcgccctgaa ggagctggac atgcacggca tcttcttcg ctactcgat 1140  
gagaccacgc tccggccact ggccgcctg cccatgtcc agactctgcg tctgcagatg 1200  
aacttcatca accaggccca gctcggcatc ttcaggcct tccctggcct gcgtacgtg 1260  
gacctgtcgg acaaccgcat cagcggagct tcggagctga cagccaccat gggggaggca 1320  
gatggagggg agaaggctctg gctgcagcct ggggacctt ctccggcccc agtggacact 1380  
cccagctctg aagacttcag gcccaactgc agcaccctca acttcacctt ggatctgtca 1440  
cggaacaacc tggtagcgt gcagcggag atgtttgcc agctctgca cctgcagtgc 1500  
ctgcgcctga gccacaactg catctcgag gcagtcaatg gctccagtt cctgccgtg 1560  
accggtctgc aggtgctaga cctgtccgc aataagctgg acctctacca cgagcactca 1620  
ttcacggagc taccgcgact ggaggccctg gacctcagct acaacagcca gccctttggc 1680  
atgcagggcg tgggccacaa cttcagcttc gtggctcacc tgcgcaccct gcgccacctc 1740  
agcctggccc acaacaacat ccacagccaa gtgtcccagc agctctgcag tacgtcgtg 1800  
cgggccttg acttcagcgg caatgcactg ggcatatgt gggccgagg agacctctat 1860  
ctgcacttct tccaaggcct gagcggtttg atctggctgg acttgtccca gaaccgctg 1920  
cacacctcc tgcggcaaac cctgcgcaac ctcccaaga gcctacaggt gctgcgtctc 1980  
cgtgacaatt acctggcctt ctttaagtgg tggagcctcc acttctgccc caaactggaa 2040



gtcctcgacc tggcaggaaa ccggtgaag gccctgacca atggcagcct gcctgctggc 2100  
 acccggtcc ggaggctgga tgcagctgc aacagcatca gcttcgtggc ccccggttc 2160  
 ttttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgccct caagacagtg 2220  
 gaccactcct ggtttggggc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280  
 cctctgcact gcgcctgtgg ggcggccttt atggacttcc tgctggaggt gcaggctgcc 2340  
 gtgcccggtc tgcccagccg ggtgaagtgt ggcagtccgg gccagctcca gggcctcagc 2400  
 atctttgcac aggacctgcg cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37  
 <211> 26  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 37  
 accttgctg ccttctacc ctgtga 26

<210> 38  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 38  
 gtccgtgtgg gccagcaca a 21

<210> 39  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 39  
 tccatgacgt ttttgatgtt 20

<210> 40  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic oligonucleotide

<400> 40  
tccataacgt ttttgatggt 20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 41  
tccatcacgt ttttgatggt 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 42  
tccattacgt ttttgatggt 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 43  
tccatggcgt ttttgatggt 20

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 44  
tccatgccgt ttttgatggt 20

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgtcgt ttttgatggt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgatgt ttttgatggt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttgatggt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttgatggt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttgatggt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 50  
tccatgacct ttttgatggt 20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 51  
tccatgactt ttttgatggt 20

<210> 52  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 52  
tccatgacgc ttttgatggt 20

<210> 53  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 53  
tccatgacga ttttgatggt 20

<210> 54  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 54  
tccatgacgg ttttgatggt 20

<210> 55  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 55  
tccatgacgt ctttgatggt 20

<210> 56  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 56  
tccatgacgt atttgatggt 20

<210> 57  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 57  
tccatgacgt gtttgatggt 20

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 58  
tcgtcgtttt gtcgttttgt cggt 24

<210> 59  
<211> 24  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic oligonucleotide

<400> 59  
tgctgctttt gtgcttttgt gctt 24

<210> 60  
<211> 20  
<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 60

tccatgacgt tcctgatgct

20

<210> 61

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 61

tccatgagct tcctgatgct

20

<210> 62

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Consensus oligopeptide

<220>

<221> MISC\_FEATURE

<222> (4)..(5)

<223> Any amino acid

<220>

<221> MISC\_FEATURE

<222> (7)..(12)

<223> Any amino acid

<220>

<221> MISC\_FEATURE

<222> (14)..(15)

<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys  
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys  
 1 5 10 15

<210> 64  
 <211> 16  
 <212> PRT  
 <213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys  
 1 5 10 15

<210> 65  
 <211> 31  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Consensus oligopeptide

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
                   20                                  25                                  30

<210> 66  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
   1                  5                                  10                                  15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr  
                   20                                  25                                  30

<210> 67  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(8)  
 <223> Any amino acid



<220>  
 <221> MISC\_FEATURE  
 <222> (10)..(10)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (14)..(22)  
 <223> Any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (25)..(30)  
 <223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Tyr  
 20 25 30

<210> 68  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His  
 1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr  
 20 25 30

<210> 69  
 <211> 31  
 <212> PRT  
 <213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

```
<400> 70
tccaggactt ctctcagggt 20
```